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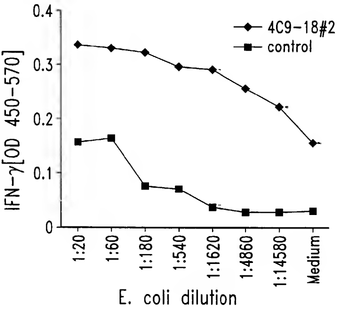
(54) Title: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION



(57) Abstract: Compounds and methods for the diagnosis and treatment of Chlamydial infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a *Chlamydia* antigen and DNA sequences encoding such polypeptides. Pharmaceutical compositions and vaccines comprising such polypeptides or DNA sequences are also provided, together with antibodies directed against such polypeptides. Diagnostic kits containing such polypeptides or DNA sequences and a suitable detection reagent may be used for the detection of Chlamydial infection in patients and in biological samples.

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COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

TECHNICAL FIELD

The present invention relates generally to the detection and treatment of Chlamydial infection. In particular, the invention is related to polypeptides comprising a *Chlamydia* antigen and the use of such polypeptides for the serodiagnosis and treatment of Chlamydial infection.

BACKGROUND OF THE INVENTION

Chlamydiae are intracellular bacterial pathogens that are responsible for a wide variety of important human and animal infections. *Chlamydia trachomatis* is one of the most common causes of sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. *Chlamydia trachomatis* may also play a role in male infertility. In 1990, the cost of treating PID in the US was estimated to be $4 billion. Trachoma, due to ocular infection with *Chlamydia trachomatis*, is the leading cause of preventable blindness worldwide. *Chlamydia pneumonia* is a major cause of acute respiratory tract infections in humans and is also believed to play a role in the pathogenesis of atherosclerosis and, in particular, coronary heart disease. Individuals with a high titer of antibodies to *Chlamydia pneumonia* have been shown to be at least twice as likely to suffer from coronary heart disease as seronegative individuals. Chlamydial infections thus constitute a significant health problem both in the US and worldwide.

Chlamydial infection is often asymptomatic. For example, by the time a woman seeks medical attention for PID, irreversible damage may have already occurred resulting in infertility. There thus remains a need in the art for improved vaccines and pharmaceutical compositions for the prevention and treatment of *Chlamydia* infections. The present invention fulfills this need and further provides other related advantages.

SUMMARY OF THE INVENTION

The present invention provides compositions and methods for the diagnosis and therapy of *Chlamydia* infection. In one aspect, the present invention

provides polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, or a variant of such an antigen. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments,, the polypeptide comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of (a) a sequence of SEQ ID NO: 358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596; (b) the complements of said sequences; and (c) sequences that hybridize to a sequence of (a) or (b) under moderate to highly stringent conditions. In specific embodiments, the polypeptides of the present invention comprise at least a portion of a *Chlamydial* protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599 and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a *Chlamydial* protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

In a related aspect, polynucleotide sequences encoding the above polypeptides, recombinant expression vectors comprising one or more of these polynucleotide sequences and host cells transformed or transfected with such expression vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising an inventive polypeptide, or, alternatively, an inventive polypeptide and a known *Chlamydia* antigen, as well as polynucleotides encoding such fusion proteins, in combination with a physiologically acceptable carrier or immunostimulant for use as pharmaceutical compositions and vaccines thereof.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody, both polyclonal and monoclonal, or antigen-binding fragment thereof that specifically binds to a *Chlamydial* protein; and (b) a physiologically acceptable carrier. Within other aspects, the present invention provides pharmaceutical compositions that comprise one or more *Chlamydia* polypeptides disclosed herein, e.g., a polypeptide according to SEQ ID NO:362-365, 386-405, 431-454, 490-515, 518-522, 560-581, and 597-599, or a polynucleotide molecule encoding

such a polypeptide, sueh as a polynucleotide according to SEQ ID NO:358-361, 366-385, 406-430, 455-489, 516-517, 523-559, and 582-596, and a physiologically acceptable carrier. The invention also provides vaccines for prophylactic and therapeutic purposes comprising one or more of the disclosed polypeptides and an immunostimulant, as defined herein, together with vaccines comprising one or more polynucleotide sequences encoding such polypeptides and an immunostimulant.

In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above pharmaceutical compositions or vaccines.

In yet a further aspect, methods for the treatment of *Chlamydia* infection in a patient are provided, the methods comprising obtaining peripheral blood mononuclear cells (PBMC) from the patient, incubating the PBMC with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated T cells and administering the incubated T cells to the patient. The present invention additionally provides methods for the treatment of *Chlamydia* infection that comprise incubating antigen presenting cells with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated antigen presenting cells and administering the incubated antigen presenting cells to the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient. In eertain cmbodiments, the antigcn presenting cells are selected from the group eonsisting of dendritic cells, macrophages, monocytes, B-cells, and fibroblasts. Compositions for the treatment of *Chlamydia* infection comprising T cells or antigen presenting cells that have been incubated with a polypeptide or polynucleotide of the present invention are also provided. Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, within other aspects, methods for removing *Chlamydial*-infected cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a *Chlamydial* protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of *Chlamydial* infection in a patient, comprising administering to a patient a biological sample treated as described above. In further aspects of the subject invention, methods and diagnostic kits are provided for detecting *Chlamydia* infection in a patient. In one embodiment, the method comprises: (a) contacting a biological sample with at least one of the polypeptides or fusion proteins disclosed herein; and (b) detecting in the sample the presence of binding agents that bind to the polypeptide or fusion protein, thereby detecting *Chlamydia* infection in the biological sample. Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. In one embodiment, the diagnostic kits comprise one or more of the polypeptides or fusion proteins disclosed herein in combination with a detection reagent. In yet another embodiment, the diagnostic kits comprise either a monoclonal antibody or a polyclonal antibody that binds with a polypeptide of the present invention.

The present invention also provides methods for detecting *Chlamydia* infection comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of a polynucleotide sequence peptide disclosed herein, or of a sequence that hybridizes thereto.

In a further aspect, the present invention provides a method for detecting *Chlamydia* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence disclosed herein, or a sequence that hybridizes thereto.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are

hereby incorporated by reference in their entirety as if each was incorporated individually.

SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined DNA sequence for the *C. trachomatis* clone 1-B1-66.

SEQ ID NO: 2 is the determined DNA sequence for the *C. trachomatis* clone 4-D7-28.

SEQ ID NO: 3 is the determined DNA sequence for the *C. trachomatis* clone 3-G3-10.

SEQ ID NO: 4 is the determined DNA sequence for the *C. trachomatis* clone 10-C10-31.

SEQ ID NO: 5 is the predicted amino acid sequence for 1-B1-66.

SEQ ID NO: 6 is the predicted amino acid sequence for 4-D7-28.

SEQ ID NO: 7 is a first predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 8 is a second predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 9 is a third predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 10 is a fourth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 11 is a fifth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 12 is the predicted amino acid sequence for 10-C10-31.

SEQ ID NO: 13 is the amino acid sequence of the synthetic peptide 1-B1-66/48-67.

SEQ ID NO: 14 is the amino acid sequence of the synthetic peptide 1-B1-66/58-77.

SEQ ID NO: 15 is the determined DNA sequence for the *C. trachomatis* serovar LGV II clone 2C7-8

SEQ ID NO: 16 is a DNA sequence of a putative open reading frame from a region of the*C. trachomatis* serovar D genome to which 2C7-8 maps

SEQ ID NO: 17 is the predicted amino acid sequence encoded by the DNA sequence of SEQ ID NO: 16

SEQ ID NO: 18 is the amino acid sequence of the synthetic peptide CtC7.8-12

SEQ ID NO: 19 is the amino acid sequence of the synthetic peptide CtC7.8-13

SEQ ID NO: 20 is the predieted amino acid sequenee encoded by a second putative open reading from *C. trachomatis* serovar D

SEQ ID NO: 21 is the determined DNA sequence for clone 4C9-18 from *C. trachomatis* LGV II

SEQ ID NO: 22 is the determined DNA sequence homologous to Lipoamide Dehydrogenase from *C. trachomatis* LGV II

SEQ ID NO: 23 is the determined DNA sequence homologous to Hypothetical protein from *C. trachomatis* LGV II

SEQ ID NO: 24 is the determined DNA sequence homologous to Ubiquinone Mehtyltransferase from *C. trachomatis* LGV II

SEQ ID NO: 25 is the determined DNA sequence for clone 4C9-18#2 BL21 pLysS from *C. trachomatis* LGV II

SEQ ID NO: 26 is the predicted amino acid sequence for 4C9-18#2 from *C. trachomatis* LGV II

SEQ ID NO: 27 is the determined DNA sequence for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 28 is the predicted amino acid sequenee for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 29 is the determined DNA sequence for Cp-S13 (CT509) from *C. pneumonia* strain TWAR

SEQ ID NO: 30 is the predicted amino acid sequence for Cp-S13 from *C. pneumonia* strain TWAR

SEQ ID NO: 31 is the amino acid sequence for a 10mer consensus peptide from CtC7.8-12 and CtC7.8-13

SEQ ID NO: 32 is the predicted amino acid sequence for clone 2C7-8 from *C. trachomatis* LGV II

SEQ ID NO: 33 is the DNA sequence corresponding to nucleotides 597304-597145 of the *C. trachomatis* serovar D genome (NCBI, BLASTN search), which shows homology to clone 2C7-8

SEQ ID NO: 34 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 33

SEQ ID NO: 35 is the DNA sequence for C.p. SWIB Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 36 is the DNA sequence for C.p. SWIB EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO : 37 is the DNA sequence for C.p. S13 Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 38 is the DNA sequence for C.p. S13 EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO: 39 is the amino acid sequence for CtSwib 52-67 peptide from *C. trachomatis* LGV II

SEQ ID NO: 40 is the amino acid sequence for CpSwib 53-68 peptide from *C. pneumonia*

SEQ ID NO: 41 is the amino acid sequence for HuSwib 288-302 peptide from Human SWI domain

SEQ ID NO: 42 is the amino acid sequence for CtSWI-T 822-837 peptide from the topoisomerase-SWIB fusion of *C. trachomatis*

SEQ ID NO: 43 is the amino acid sequence for CpSWI-T 828-842 peptide from the topoisomerase-SWIB fusion of *C. pneumonia*

SEQ ID NO: 44 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19783.3,jen.seq(1>509)CTL2#11-3', representing the 3' end.

SEQ ID NO: 45 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19783.4,jen.seq(1>481)CTL2#11-5', representing the 5' end.

SEQ ID NO: 46 is the determined DNA sequence for the *C. trachomatis* LGV II clone19784CTL2_12consensus.seq(1>427)CTL2#12.

SEQ ID NO: 47 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19785.4,jen.seq(1>600)CTL2#16-5', representing the 5' end.

SEQ ID NO: 48 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19786.3,jen.seq(1>600)CTL2#18-3', representing the 3' end.

SEQ ID NO: 49 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19786.4,jen.seq(1>600)CTL2#18-5', representing the 5' end.

SEQ ID NO: 50 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19788CTL2_21consensus.seq(1>406)CTL2#21.

SEQ ID NO: 51 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19790CTL2_23consensus.seq(1>602)CTL2#23.

SEQ ID NO: 52 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19791CTL2_24consensus.seq(1>145)CTL2#24.

SEQ ID NO: 53 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#4.

SEQ ID NO: 54 is the determined DNA sequence for the *C. trachomatis* LGV II clone CTL2#8b.

SEQ ID NO: 55 is the determined DNA sequence for the *C. trachomatis* LGV II clone15-G1-89, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 56 is the determined DNA sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 57 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-G3-83, sharing homology to the hypothetical protein CT622.

SEQ ID NO: 58 is the determined DNA sequence for the *C. trachomatis* LGV II clone 12-B3-95, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 59 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H4-28, sharing homology to the dnaK gene CT396.

SEQ ID NO: 60 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-H3-68, sharing partial homology to the PGP6-D virulence protein and L1 ribosomal gene CT318.

SEQ ID NO: 61 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G1-34, sharing partial homology to the malate dehydrogenase gene CT376 and to the glycogen hydrolase gene CT042.

SEQ ID NO: 62 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-G10-46, sharing homology to the hypothetical protein CT610.

SEQ ID NO: 63 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-C12-91, sharing homology to the OMP2 gene CT443.

SEQ ID NO: 64 is the determined DNA sequence for the *C. trachomatis* LGV II clone 11-A3-93, sharing homology to the HAD superfamily gene CT103.

SEQ ID NO: 65 is the determined amino acid sequence for the *C. trachomatis* LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 66 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#9.

SEQ ID NO: 67 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#7.

SEQ ID NO: 68 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#6.

SEQ ID NO: 69 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#5.

SEQ ID NO: 70 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#2.

SEQ ID NO: 71 is the determined DNA sequence for the *C. trachomatis* LGV II clone CtL2#1.

SEQ ID NO: 72 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 23509.2CtL2#3-5', representing the 5' end.

SEQ ID NO: 73 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 23509.1CtL2#3-3', representing the 3' end.

SEQ ID NO: 74 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 22121.2CtL2#10-5', representing the 5' end.

SEQ ID NO: 75 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 22121.1CtL2#10-3', representing the 3' end.

SEQ ID NO: 76 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19787.6CtL2#19-5', representing the 5' end.

SEQ ID NO: 77 is the determined DNA sequence for the *C. pneumoniae* LGV II clone CpS13-His.

SEQ ID NO: 78 is the determined DNA sequence for the *C. pneumoniae* LGV II clone Cp_SWIB-His.

SEQ ID NO: 79 is the determined DNA sequence for the *C. trachomatis* LGV II clone 23-G7-68, sharing partial homology to the L11, L10 and L1 ribosomal protein.

SEQ ID NO: 80 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-F8-91, sharing homology to the pmpC gene.

SEQ ID NO: 81 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-E8-95, sharing homology to the CT610-CT613 genes.

SEQ ID NO: 82 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-57, sharing homology to the CT858 and recA genes.

SEQ ID NO: 83 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-F12-53, sharing homology to the CT445 gene encoding glutamyl tRNA synthetase.

SEQ ID NO: 84 is the determined DNA sequence for the *C. trachomatis* LGV II clone 19-A5-54, sharing homology to the eryptic plasmid gene.

SEQ ID NO: 85 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E11-72, sharing partial homology to the OppC_2 and pmpD genes.

SEQ ID NO: 86 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C1-77, sharing partial homology to the CT857 and CT858 open reading frames.

SEQ ID NO: 87 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-H2-76, sharing partial homology to the pmpD and SycE genes, and to the CT089 ORF.

SEQ ID NO: 88 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-A3-26, sharing homology to the CT858 ORF.

SEQ ID NO: 89 is the determined amino acid sequence for the *C. pnuemoniae* clone Cp_SWIB-His.

SEQ ID NO: 90 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_LPDA_FL.

SEQ ID NO: 91 is the determined amino acid sequence for the *C. pnuemoniae* clone CpS13-His.

SEQ ID NO: 92 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2_TSA_FL.

SEQ ID NO: 93 is the amino acid sequence for Ct-Swib 43-61 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 94 is the amino acid sequence for Ct-Swib 48-67 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 95 is the amino acid sequence for Ct-Swib 52-71 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 96 is the amino acid sequence for Ct-Swib 58-77 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 97 is the amino acid sequence for Ct-Swib 63-82 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 98 is the amino acid sequence for Ct-Swib 51-66 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 99 is the amino acid sequence for Cp-Swib 52-67 peptide from *C. pneumonia*.

SEQ ID NO: 100 is the amino acid sequence for Cp-Swib 37-51 peptide from *C. pneumonia*.

SEQ ID NO: 101 is the amino acid sequence for Cp-Swib 32-51 peptide from *C. pneumonia*.

SEQ ID NO: 102 is the amino acid sequence for Cp-Swib 37-56 peptide from *C. pneumonia*.

SEQ ID NO: 103 is the amino acid sequence for Ct-Swib 36-50 peptide from *C. trachomatis*.

SEQ ID NO: 104 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 105 is the amino acid sequence for Ct-S13 60-80 peptide from *C. trachomatis*.

SEQ ID NO: 106 is the amino acid sequence for Ct-S13 1-20 peptide from *C. trachomatis*.

SEQ ID NO: 107 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 108 is the amino acid sequence for Ct-S13 56-75 peptide from *C. trachomatis*.

SEQ ID NO: 109 is the amino acid sequence for Cp-S13 56-75 peptide from *C. pneumoniae*.

SEQ ID NO: 110 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-G12-60, containing partial open reading frames for hypothetical proteins CT875, CT229 and CT228.

SEQ ID NO: 111 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-B3-53, sharing homology to the CT110 ORF of GroEL.

SEQ ID NO: 112 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-A1-49, sharing partial homology to the CT660 and CT659 ORFs.

SEQ ID NO: 113 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E2-9, sharing partial homology to the CT611 and CT 610 ORFs.

SEQ ID NO: 114 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C10-31, sharing partial homology to the CT858 ORF.

SEQ ID NO: 115 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-C7-8, sharing homology to the dnaK-like gene.

SEQ ID NO: 116 is the determined DNA sequence for the *C. trachomatis* LGV II clone 20-G3-45, containing part of the pmpB gene CT413.

SEQ ID NO: 117 is the determined DNA sequence for the *C. trachomatis* LGV II clone 18-C5-2, sharing homology to the S1 ribosomal protein ORF.

SEQ ID NO: 118 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C5-19, containing part of the ORFs for CT431 and CT430.

SEQ ID NO: 119 is the determined DNA sequence for the *C. trachomatis* LGV II clone 16-D4-22, contains partial sequences of ORF3 and ORF4 of the plasmid for growth within mammalian cells.

SEQ ID NO: 120 is the determined full-length DNA sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 121 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 122 is the determined full-length DNA sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 123 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 124 is the determined full-length DNA sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 125 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 126 is the determined full-length DNA sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 127 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 128 is the determined full-length DNA sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 129 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 130 is the determined full-length DNA sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 131 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 132 is the determined full-length DNA sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

SEQ ID NO: 133 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar L3 Cap1 gene CT529.

SEQ ID NO: 134 is the determined full-length DNA sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

SEQ ID NO: 135 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar Ba Cap1 gene CT529.

SEQ ID NO: 136 is the determined full-length DNA sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

SEQ ID NO: 137 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar MOPN Cap1 gene CT529.

SEQ ID NO: 138 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #124-139 of *C. trachomatis* serovar L2.

SEQ ID NO: 139 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #132-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 140 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-155 of *C. trachomatis* serovar L2.

SEQ ID NO: 141 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #146-163 of *C. trachomatis* serovar L2.

SEQ ID NO: 142 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #154-171 of *C. trachomatis* serovar L2.

SEQ ID NO: 143 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #162-178 of *C. trachomatis* serovar L2.

SEQ ID NO: 144 is the determined amino acid sequenee for the Cap1 CT529 ORF peptide #138-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 145 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #139-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 146 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #140-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 147 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-146 of *C. trachomatis* serovar L2.

SEQ ID NO: 148 is the determined amino acid sequenee for the Cap1 CT529 ORF peptide #138-145 of *C. trachomatis* serovar L2.

SEQ ID NO: 149 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # F140->I of *C. trachomatis* serovar L2.

SEQ ID NO: 150 is the determined amino acid sequenee for the Cap1 CT529 ORF peptide # #S139>Ga of *C. trachomatis* serovar L2.

SEQ ID NO: 151 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Gb of *C. trachomatis* serovar L2.

SEQ ID NO: 152 is the determined amino acid sequence for the peptide # 2 C7.8-6 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 153 is the determined amino acid sequence for the peptide # 2 C7.8-7 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 154 is the determined amino acid sequence for the peptide # 2 C7.8-8 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 155 is the determined amino acid sequence for the peptide # 2 C7.8-9 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 156 is the determined amino acid sequence for the peptide # 2 C7.8-10 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 157 is the determined amino acid sequence for the 53 amino acid residue peptide of the 216aa ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 158 is the determined amino acid sequence for the 52 amino acid residue peptide of the CT529 ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 159 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 160 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 161 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 for serovars other than L2 and MOPN.

SEQ ID NO: 162 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovars other than L2 and MOPN.

SEQ ID NO: 163 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 164 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 165 is the determined DNA sequence for the 5' (forward) primer for pBIB-KS.

SEQ ID NO: 166 is the determined DNA sequence for the 5' (reverse) primer for pBIB-KS.

SEQ ID NO: 167 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar L2.

SEQ ID NO: 168 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar D.

SEQ ID NO: 169 is the determined full-length DNA sequence for the *C. trachomatis* pmpI (CT874) gene.

SEQ ID NO: 170 is the determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 171 is the determined full-length DNA sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 172 is the determined full-length DNA sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 173 is the determined full-length DNA sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 174 is the determined full-length DNA sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 175 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 176 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 177 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 178 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 179 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 180 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 181 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 182 is a subsequently determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 183 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 184 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 185 is a second determined DNA sequenee representing the amino terminus minus the signal sequnce for the *C. trachomatis* pmpD gene.

SEQ ID NO: 186 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 187 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 188 is the determined DNA sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 189 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 190 is subsequently predicted amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 191 is the predicted amino acid sequenee minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 192 is a first predicted amino acid sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 193 is a second predicted amino acid sequence representing the Amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 194 is a first predicted amino acid sequence representing the Carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 195 is a second predicted amino acid sequence representing the Amino terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 196 is the predicted amino acid sequenee representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 197 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaceine veetor.

SEQ ID NO: 198 is the determined DNA sequence for the 3' oligo primer for eloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 199 is the determined DNA sequenee for the insertion sequence for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 200 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine veetor.

SEQ ID NO: 201 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 202 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 203 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 204 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 205 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 206 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 207 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 208 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 209 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 210 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 211 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 212 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 213 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 214 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 215 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 216 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 217 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 218 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 219 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 220 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 221 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 222 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 223 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 224 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 1-20.

SEQ ID NO: 225 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 6-25.

SEQ ID NO: 226 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 12-31.

SEQ ID NO: 227 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 17-36.

SEQ ID NO: 228 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 22-41.

SEQ ID NO: 229 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 27-46.

SEQ ID NO: 230 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 42-61.

SEQ ID NO: 231 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 46-65.

SEQ ID NO: 232 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 51-70.

SEQ ID NO: 233 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 56-75.

SEQ ID NO: 234 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 61-80.

SEQ ID NO: 235 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 66-87.

SEQ ID NO: 236 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 103-122.

SEQ ID NO: 237 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 108-127.

SEQ ID NO: 238 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 113-132.

SEQ ID NO: 239 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 118-137.

SEQ ID NO: 240 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 123-143.

SEQ ID NO: 241 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 128-147.

SEQ ID NO: 242 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 133-152.

SEQ ID NO: 243 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 137-156.

SEQ ID NO: 244 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 142-161.

SEQ ID NO: 245 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 147-166.

SEQ ID NO: 246 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 152-171.

SEQ ID NO: 247 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 157-176.

SEQ ID NO: 248 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 162-181.

SEQ ID NO: 249 is the determined amino acid sequenee for the *C. trachomatis* OMCB peptide 167-186.

SEQ ID NO: 250 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-190.

SEQ ID NO: 251 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 175-186.

SEQ ID NO: 253 is the determined amino acid sequence for the *C. pneumoniae* OMCB peptide 185-198.

SEQ ID NO: 254 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 96-115.

SEQ ID NO: 255 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 101-120.

SEQ ID NO: 256 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 106-125.

SEQ ID NO: 257 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 111-130.

SEQ ID NO: 258 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 116-135.

SEQ ID NO: 259 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 121-140.

SEQ ID NO: 260 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 126-145.

SEQ ID NO: 261 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 131-150.

SEQ ID NO: 262 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 136-155.

SEQ ID NO: 263 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 264 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 265 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 266 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 267 is the determined DNA sequence for the *C. trachomatis* clone 17-G4-36 sharing homology to part of the ORF of DNA-dirrected RNA polymerase beta subunit- CT315 in serD.

SEQ ID NO: 268 is the determined DNA sequence for the partial sequence of the *C. trachomatis* CT016 gene in clone 2E10.

SEQ ID NO: 269 is the determined DNA sequence for the partial sequence of the *C. trachomatis* tRNA syntase gene in clone 2E10.

SEQ ID NO: 270 is the determined DNA sequence for the partial sequence for the *C. trachomatis* clpX gene in clone 2E10.

SEQ ID NO: 271 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 5'end.

SEQ ID NO: 272 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 3'end.

SEQ ID NO: 273 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-28.

SEQ ID NO: 274 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-27.

SEQ ID NO: 275 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-26.

SEQ ID NO: 276 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-24.

SEQ ID NO: 277 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-23.

SEQ ID NO: 278 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-21.

SEQ ID NO: 279 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-18.

SEQ ID NO: 280 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-17.

SEQ ID NO: 281 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 5' end.

SEQ ID NO: 282 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 3' end.

SEQ ID NO: 283 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-13.

SEQ ID NO: 284 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-10.

SEQ ID NO: 285 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-8.

SEQ ID NO: 286 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 5' end.

SEQ ID NO: 287 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 3' end.

SEQ ID NO: 288 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-5.

SEQ ID NO: 289 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-2.

SEQ ID NO: 290 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-1.

SEQ ID NO: 291 is the determined full-length DNA sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 292 is the predicted full-length amino acid sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 293 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 294 is the amino acid sequence of an open reading frame of clone CT603.

SEQ ID NO: 295 is the amino acid sequence of a first open reading frame of clone CT875.

SEQ ID NO: 296 is the amino acid sequence of a second open reading frame of clone CT875.

SEQ ID NO: 297 is the amino acid sequence of a first open reading frame of clone CT858.

SEQ ID NO: 298 is the amino acid sequence of a second open reading frame of clone CT858.

SEQ ID NO: 299 is the amino acid sequence of an open reading frame of clone CT622.

SEQ ID NO: 300 is the amino acid sequence of an open reading frame of clone CT610.

SEQ ID NO: 301 is the amino acid sequence of an open reading frame of clone CT396.

SEQ ID NO: 302 is the amino acid sequence of an open reading frame of clone CT318.

SEQ ID NO: 304 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125 having a modified N-terminal sequence (6-His tag).

SEQ ID NO: 305 is the amino acid sequence for *C. trachomatis*, serovar L2 rCt529c1-125.

SEQ ID NO: 306 is the sense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 307 is the antisense primer used in the synthesis of the PmpA(N-term) fusion protein.

SEQ ID NO: 308 is the DNA sequence encoding the PmpA(N-term) fusion protein.

SEQ ID NO: 309 is the amino acid sequence of the PmpA(N-term) fusion protein.

SEQ ID NO: 310 is the sense primer used in the synthesis of the PmpA(C-term) fusion protein.

SEQ ID NO: 311 is the antisense primer used in the synthesis of the PmpA(C-term) fusion protein.

SEQ ID NO: 312 is the DNA sequence encoding the PmpA(C-term) fusion protein.

SEQ ID NO: 313 is the amino acid sequence of the PmpA(C-term) fusion protein.

SEQ ID NO: 314 is the sense primer used in the synthesis of the PmpF(N-term) fusion protein.

SEQ ID NO: 315 is the antisense primer used in the synthesis of the PmpF(N-term) fusion protein.

SEQ ID NO: 316 is the DNA sequence encoding the PmpF(N-term) fusion protein.

SEQ ID NO: 317 is the amino acid sequence of the PmpF(N-term) fusion protein.

SEQ ID NO: 318 is the sense primer used in the synthesis of the PmpF(C-term) fusion protein.

SEQ ID NO: 319 is the antisense primer used in the synthesis of the PmpF(C-term) fusion protein.

SEQ ID NO: 320 is the DNA sequence encoding the PmpF(C-term) fusion protein.

SEQ ID NO: 321 is the amino acid sequence of the PmpF(C-term) fusion protein.

SEQ ID NO: 322 is the sense primer used in the synthesis of the PmpH (CT412) (N-term) fusion protein.

SEQ ID NO: 323 is the antisense primer used in the synthesis of the PmpH(N-term) fusion protein.

SEQ ID NO: 324 is the DNA sequence encoding the PmpH(N-term) fusion protein.

SEQ ID NO: 325 is the amino acid sequence of the PmpH(N-term) fusion protein.

SEQ ID NO: 326 is the sense primer used in the synthesis of the PmpH(C-term) fusion protein.

SEQ ID NO: 327 is the antisense primer used in the synthesis of the PmpH(C-term) fusion protein.

SEQ ID NO: 328 is the DNA sequence encoding the PmpH(C-term) fusion protein.

SEQ ID NO: 329 is the amino acid sequence of the PmpH(C-term) fusion protein.

SEQ ID NO: 330 is the sense primer used in the synthesis of the PmpB(1) fusion protein.

SEQ ID NO: 331 is the antisense primer used in the synthesis of the PmpB(1) fusion protein.

SEQ ID NO: 332 is the DNA sequence encoding the PmpB(1) fusion protein.

SEQ ID NO: 333 is the amino acid sequence of the PmpB(1) fusion protein.

SEQ ID NO: 334 is the sense primer used in the synthesis of the PmpB(2) fusion protein.

SEQ ID NO: 335 is the antisense primer used in the synthesis of the PmpB(2) fusion protein.

SEQ ID NO: 336 is the DNA sequence encoding the PmpB(2) fusion protein.

SEQ ID NO: 337 is the amino acid sequence of the PmpB(2) fusion protein.

SEQ ID NO: 338 is the sense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 339 is the antisense primer used in the synthesis of the PmpB(3) fusion protein.

SEQ ID NO: 340 is the DNA sequence encoding the PmpB(3) fusion protein.

SEQ ID NO: 341 is the amino acid sequence of the PmpB(3) fusion protein.

SEQ ID NO: 342 is the sense primer used in the synthesis of the PmpB(4) fusion protein.

SEQ ID NO: 343 is the antisense primer used in the synthesis of the PmpB(4) fusion protein.

SEQ ID NO: 344 is the DNA sequence encoding the PmpB(4) fusion protein.

SEQ ID NO: 345 is the amino acid sequence of the PmpB(4) fusion protein.

SEQ ID NO: 346 is the sense primer used in the synthesis of the PmpC(1) fusion protein.

SEQ ID NO: 347 is the antisense primer used in the synthesis of the PmpC(1) fusion protein.

SEQ ID NO: 348 is the DNA sequence encoding the PmpC(1) fusion protein.

SEQ ID NO: 349 is the amino acid sequence of the PmpC(1) fusion protein.

SEQ ID NO: 350 is the sense primer used in the synthesis of the PmpC(2) fusion protein.

SEQ ID NO: 351 is the antisense primer used in the synthesis of the PmpC(2) fusion protein.

SEQ ID NO: 352 is the DNA sequence encoding the PmpC(2) fusion protein.

SEQ ID NO: 353 is the amino acid sequence of the PmpC(2) fusion protein.

SEQ ID NO: 354 is the sense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 355 is the antisense primer used in the synthesis of the PmpC(3) fusion protein.

SEQ ID NO: 356 is the DNA sequence encoding the PmpC(3) fusion protein.

SEQ ID NO: 357 is the amino acid sequence of the PmpC(3) fusion protein.

SEQ ID NO: 358 is the DNA sequence of the oppA1 protein, devoid of the first trans-membrane domain.

SEQ ID NO: 359 is the full length DNA sequence of CT139.

SEQ ID NO: 360 is the full length DNA sequence of ORF-3.

SEQ ID NO: 361 is the full length DNA sequence of CT611.

SEQ ID NO: 362 is the amino acid sequence of oppA1 starting from amino acid 22.

SEQ ID NO: 363 is the amino acid sequence of CT139.

SEQ ID NO: 364 is the amino acid sequence of ORF-3.

SEQ ID NO: 365 is the amino acid sequence of CT611.

SEQ ID NO: 366 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

SEQ ID NO: 367 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 368 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 369 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 370 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 371 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 372 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 373 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 374 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 375 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 376 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 377 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 378 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 379 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 380 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia traehomatis gene CT604.

SEQ ID NO: 381 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia traehomatis gene CT042.

SEQ ID NO: 382 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 383 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 384 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 385 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 386 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0275, of the Chlamydia trachomatis gene CT190.

SEQ ID NO: 387 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0407, of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 388 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0720, of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 389 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0716, of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 390 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0519, of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 391 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0520, of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 392 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0078, of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 393 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0628, of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 394 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0540, of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 395 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, pmp20, of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 396 sets forth the amino aeid sequence for the Chlamydia pneumoniae homologue, CPn0081, of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 397 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0761, of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 398 sets forth the amino acid sequenee for the Chlamydia pneumoniae homologue, CPn0557, of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 399 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0833, of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 400 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0134, of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 401 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0388, of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 402 sets forth the amino aeid sequence for the Chlamydia pneumoniae homologue, CPn1028, of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 403 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0875, of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 404 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0908, of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 405 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0728, of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 406 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT287.

SEQ ID NO: 407 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT858.

SEQ ID NO: 408 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 409 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 410 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 411 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 412 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 413 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 414 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 415 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 416 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 417 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 418 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 419 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 420 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 421 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 422 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT396.

SEQ ID NO: 423 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 424 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 425 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 426 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT104.

SEQ ID NO: 427 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 428 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 429 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 430 sets forth the full-length serovar D DNA sequence of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 431 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT858.

SEQ ID NO: 432 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT764.

SEQ ID NO: 433 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT734.

SEQ ID NO: 434 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT660.

SEQ ID NO: 435 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT659.

SEQ ID NO: 436 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT622.

SEQ ID NO: 437 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT610.

SEQ ID NO: 438 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT604.

SEQ ID NO: 439 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT557.

SEQ ID NO: 440 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT509.

SEQ ID NO: 441 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT443.

SEQ ID NO: 442 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT431.

SEQ ID NO: 443 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT430.

SEQ ID NO: 444 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT414.

SEQ ID NO: 445 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT413.

SEQ ID NO: 446 sets forth the full-length serovar D amino acid sequence of the Chlamydia trachomatis gene CT396.

SEQ ID NO: 447 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT376.

SEQ ID NO: 448 sets forth the full length serovar D amino aeid sequence of the Chlamydia trachomatis gene CT318.

SEQ ID NO: 449 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT315.

SEQ ID NO: 450 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT104.

SEQ ID NO: 451 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT103.

SEQ ID NO: 452 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 453 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 454 sets forth the full length serovar D amino acid sequence of the Chlamydia trachomatis gene CT042.

SEQ ID NO: 455 corresponds to the DNA sequence of CPn0894, which is the CP homologue of CT751 (amn), which was identified in clones CTL2-1, and CTL2-5.

SEQ ID NO: 456 corresponds to the DNA sequence of CPn0074, which is the CP homologue of CT322 (tuf), which was identified in clone CTL2-2.

SEQ ID NO: 457 corresponds to the DNA sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 458 corresponds to the DNA sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

SEQ ID NO: 459 corresponds to the DNA sequence of CPn0120, which is the CP homologue of CT030 (gmK), which was identified in clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 460 corresponds to the DNA sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

SEQ ID NO: 461 corresponds to the DNA sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

SEQ ID NO: 462 corresponds to the DNA sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

SEQ ID NO: 463 corresponds to the DNA sequence of CPn0394, which is the CP homologue of CT256 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 464 corresponds to the DNA sequence of CPn0395, which is the CP homologue of CT257 which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 465 corresponds to the DNA sequence of CPn0487, which is the CP homologue of CT384 which was identified in clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 466 corresponds to the DNA sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 467 corresponds to the DNA sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

SEQ ID NO: 468 corresponds to the DNA sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 469 corresponds to the DNA sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

SEQ ID NO: 470 corresponds to the DNA sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 471 corresponds to the DNA sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

SEQ ID NO: 472 corresponds to the DNA sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

SEQ ID NO: 473 corresponds to the DNA sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

SEQ ID NO: 474 corresponds to the DNA sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

SEQ ID NO: 475 corresponds to the DNA sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 476 corresponds to the DNA sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

SEQ ID NO: 477 corresponds to the DNA sequence of CPn0984, which is the CP homologue of CT827 (nrdA), which was identified in clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 478 corresponds to the DNA sequence of CPn0985 which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

SEQ ID NO: 479 corresponds to the DNA sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone CTL2gam18.

SEQ ID NO: 480 corresponds to the DNA sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

SEQ ID NO: 481 corresponds to the DNA sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

SEQ ID NO: 482 corresponds to the DNA sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

SEQ ID NO: 483 corresponds to the DNA sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone CTL2gam24.

SEQ ID NO: 484 corresponds to the DNA sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

SEQ ID NO: 485 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

SEQ ID NO: 486 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

SEQ ID NO: 487 corresponds to the DNA sequence of CPn-ORF5, which is the CP homologue of CT-ORF3, which was identified in clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

SEQ ID NO: 488 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

SEQ ID NO: 489 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

SEQ ID NO: 490 corresponds to the amino acid sequence of CPn0894, which is the CP homologue of CT751 (amn), which was identified in clones CTL2-1 and CTL2-5.

SEQ ID NO: 491 corresponds to the amino acid sequence of CPn0074, which is the CP homologue of CT332 (tuf), which was identified in clone CTL2-2.

SEQ ID NO: 492 corresponds to the amino acid sequence of CPn0122, which is the CP homologue of CT032 (metG), which was identified in clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 493 corresponds to the amino acid sequence of CPn0121, which is the CP homologue of CT031, which was identified in clone CTL2-3(5')(3').

SEQ ID NO: 494 corresponds to the amino acid sequence of CPn0120 which is the CP homologue of CT030 (gmK) which was identified in clones CTL2-3 (3') and CTL2-21.

SEQ ID NO: 495 corresponds to the amino acid sequence of CPn0359, which is the CP homologue of CT064 (lepA), which was identified in clone CTL2gam5.

SEQ ID NO: 496 corresponds to the amino acid sequence of CPn0414, which is the CP homologue of CT265 (accA), which was identified in clone CTL2-6.

SEQ ID NO: 497 corresponds to the amino acid sequence of CPn0413, which is the CP homologue of CT264 (msbA), which was identified in clone CTL2-6.

SEQ ID NO: 498 corresponds to the amino acid sequence of CPn0394, which is the CP homologue of CT256, which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 499 corresponds to the amino acid sequence of CPn0395, which is the CP homologue of CT257, which was identified in clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 500 eorresponds to the amino acid sequence of CPn0487, which is the CP homologue of CT384, which was identified in clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 501 corresponds to the amino acid sequence of CPn0592, which is the CP homologue of CT473, which was identified in clone CTL2-8b.

SEQ ID NO: 502 corresponds to the amino acid sequence of CPn0593, which is the CP homologue of CT474, which was identified in clone CTL2-8b.

SEQ ID NO: 503 corresponds to the amino acid sequence of CPn0197, which is the CP homologue of CT139 (oppA1), which was identified in clone CTL2-8b.

SEQ ID NO: 504 corresponds to the amino acid sequence of CPn0363, which is the CP homologue of CT060 (flhA), which was identified in clone CTL2-8b.

SEQ ID NO: 505 corresponds to the amino acid sequence of CPn0301, which is the CP homologue of CT242, which was identified in clone CTL2gam8.

SEQ ID NO: 506 corresponds to the amino acid sequence of CPn0302, which is the CP homologue of CT243 (lpxD), which was identified in clone CTL2gam8.

SEQ ID NO: 507 corresponds to the amino acid sequence of CPn0324, which is the CP homologue of CT089 (lcrE), which was identified in clones CTL2-9, CTL2gam1, CTL2gam17 and CTL2-19(5').

SEQ ID NO: 508 corresponds to the amino acid sequence of CPn0761, which is the CP homologue of CT610, which was identified in clone CTL2-10(5')(3').

SEQ ID NO: 509 corresponds to the amino acid sequence of CPn0760, which is the CP homologue of CT611, which was identified in clone CTL2-10(5').

SEQ ID NO: 510 corresponds to the amino acid sequence of CPn0329, which is the CP homologue of CT154, which was identified in clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 511 corresponds to the amino acid sequence of CPn0990, which is the CP homologue of CT833 (infC), which was identified in clone CTL2-12.

SEQ ID NO: 512 corresponds to the amino acid sequence of CPn-ORF5, which is the CP homologue of CT ORF3, which was identified in clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5'), and CTL2-23.

SEQ ID NO: 513 corresponds to the amino acid sequence of CPn0984, which is the CP homologue of CT827 (nrdA) which was identified in clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 514 corresponds to the amino acid sequence of CPn0985, which is the CP homologue of CT828 (nrdB) which was identified in clones CTL2-16(3') CTL2gam15(3').

SEQ ID NO: 515 corresponds to the amino acid sequence of CPn0349, which is the CP homologue of CT067 (ytgA), which was identified in clone CTL2gam18.

SEQ ID NO: 516 corresponds to the DNA sequence of CPn-ORF6, which is the CP homologue of CT-ORF4, which was identified in clone CTL2-18(3').

SEQ ID NO: 517 corresponds to the DNA sequence of CP-ORF7, which is the CP homologue of CT-ORF5, which was identified in clone CTL2-18(3').

SEQ ID NO: 518 corresponds to the amino acid sequence of CPn0326, which is the CP homologue of CT087 (malQ), which was identified in clone CTL2-19(5').

SEQ ID NO: 519 corresponds to the amino acid sequence of CPn0325, which is the CP homologue of CT088 (sycE), which was identified in clone CTL2-19(5').

SEQ ID NO: 520 corresponds to the amino acid sequence of CPn0793, which is the CP homologue of CT588 (rbsu), which was identified in clone CTL2gam23.

SEQ ID NO: 521 corresponds to the amino acid sequence of CPn0199, which is the CP homologue of CT199 (oppB1), which was identified in clone CTL2gam24.

SEQ ID NO: 522 corresponds to the amino acid sequence of CPn0666, which is the CP homologue of CT545 (dnaE), which was identified in clone CTL2-24.

SEQ ID NO: 523 corresponds to the DNA sequence of CPn0065, which is the CP homologue of CT288, which was identified in clone CTL2gam27.

SEQ ID NO: 524 corresponds to the DNA sequence of CPn0444, which is the CP homologue of CT413 (pmpB), which was identified in clone CTL2gam30(5')(3').

SEQ ID NO: 525 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

SEQ ID NO: 526 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

SEQ ID NO: 527 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 528 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

SEQ ID NO: 529 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 530 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

SEQ ID NO: 531 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

SEQ ID NO: 532 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

SEQ ID NO: 533 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 534 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 535 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 536 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

SEQ ID NO: 537 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

SEQ ID NO: 538 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

SEQ ID NO: 539 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 540 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

SEQ ID NO: 541 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

SEQ ID NO: 542 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 543 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

SEQ ID NO: 544 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 545 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 546 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

SEQ ID NO: 547 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrdA) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 548 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrdB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 549 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (ytgA) identified from the clone CTL2gam18.

SEQ ID NO: 550 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

SEQ ID NO: 551 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 552 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

SEQ ID NO: 553 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

SEQ ID NO: 554 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

SEQ ID NO: 555 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

SEQ ID NO: 556 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 557 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

SEQ ID NO: 558 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3').

SEQ ID NO: 559 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

SEQ ID NO: 560 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT751 (amn) identified from the clones CTL2-1 and CTL2-5.

SEQ ID NO: 561 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT322 (tuff) identified from the clone CTL2-2.

SEQ ID NO: 562 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT032 (metG) identified from the clones CTL2gam2, CTL2-3(5') and CTL2-4.

SEQ ID NO: 563 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT031 identified from the clone CTL2-3(5')(3').

SEQ ID NO: 564 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT030 (gmK) identified from the clones CTL2-3(3') and CTL2-21.

SEQ ID NO: 565 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT064 (lepA) identified from the clone CTL2gam5.

SEQ ID NO: 566 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT265 (accA) identified from the clone CTL2-6.

SEQ ID NO: 567 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT624 (msbA) identified from the clones CTL2-6.

SEQ ID NO: 568 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT256 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 569 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT257 identified from the clones CTL2gam6(5') and CTL2-11(5').

SEQ ID NO: 570 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT384 identified from the clones CTL2gam6(3') and CTL2-11(3').

SEQ ID NO: 571 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT473 identified from the clone CTL2-8b.

SEQ ID NO: 572 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT474 identified from the clones CTL2-8b.

SEQ ID NO: 573 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT139 (oppA1) identified from the clones CTL2-8b.

SEQ ID NO: 574 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT060 (flhA) identified from the clone CTL2-8b.

SEQ ID NO: 575 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT242 identified from the clone CTL2gam8.

SEQ ID NO: 576 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT243 (lpxD) identified from the clone CTL2gam8.

SEQ ID NO: 577 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT089 identified from the clones CTL2-9, CTL2gam1, CTL2gam17, and CTL2-19(5').

SEQ ID NO: 578 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT610 identified from the clone CTL2-10 (5')(3').

SEQ ID NO: 579 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT611 identified from the clone CTL2-10(5').

SEQ ID NO: 580 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT154 identified from the clones CTL2gam10 and CTL2gam21.

SEQ ID NO: 581 sets forth the full-length *C. trachomatis* serovar D amino acid sequence homologous to the *C. trachomatis* LGV II sequence for CT833 (infC) identified from the clone CTL2-12.

SEQ ID NO: 582 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF3 identified from the clones CTL2gam15(5'), CTL2-16(5'), CTL2-18(5') and CTL2-23.

SEQ ID NO: 583 sets forth thc full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT827 (nrdA) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 584 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT828 (nrdB) identified from the clones CTL2-16(3') and CTL2gam15(3').

SEQ ID NO: 585 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT067 (ytgA) identified from the clone CTL2gam18.

SEQ ID NO: 586 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for pCT-ORF4 identified from the clone CTL2-18(3')

SEQ ID NO: 587 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT-ORF5 identified from the clones CTL2-18(3').

SEQ ID NO: 588 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT087 identified from the clone CTL2-19(5').

SEQ ID NO: 589 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT088 (sycE) identified from the clones CTL2-19(5').

SEQ ID NO: 590 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT588 (rsbu) identified from the clone CTL2gam23.

SEQ ID NO: 591 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT199 (oppB1) identified from the clone CTL2gam24.

SEQ ID NO: 592 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT545 (dnaE) identified from the clone CTL2-4.

SEQ ID NO: 593 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT288 identified from the clones CTL2gam27.

SEQ ID NO: 594 sets forth the full-length *C. trachomatis* serovar D DNA sequence homologous to the *C. trachomatis* LGV II sequence for CT413 (pmpB) identified from the clone CTL2gam30(5')(3').

SEQ ID NO: 595 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 596 sets forth the DNA sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 597 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0406, of the Chlamydia trachomatis gene CT102.

SEQ ID NO: 598 sets forth the amino acid sequence for the Chlamydia pneumoniae homologue, CPn0315, of the Chlamydia trachomatis gene CT098.

SEQ ID NO: 599 sets forth the amino acid sequence for Chlamydia trachomatis serovar D CT287 protein.

DESCRIPTION OF THE FIGURES

Fig. 1 illustrates induction of INF-γ from a *Chlamydia*-specific T cell line activated by target cells expressing clone 4C9-18#2.

Fig. 2 illustrates retroviral vectors pBIB-KS1,2,3 modified to contain a Kosak translation initiation site and stop codons.

Fig. 3 shows specific lysis in a chromium release assay of P815 cells pulsed with *Chlamydia* peptides CtC7.8-12 (SEQ ID NO: 18) and CtC7.8-13 (SEQ ID NO: 19).

Fig. 4 shows antibody isotype titers in C57Bl/6 mice immunized with *C. trachomatis* SWIB protein.

Fig. 5 shows *Chlamydia*-specific T-cell proliferative responses in splenocytes from C3H mice immunized with *C. trachomatis* SWIB protein.

Fig. 6 illustrates the 5' and 3' primer sequences designed from *C. pneumoniae* which were used to isolate the SWIB and S13 genes from *C. pneumoniae*.

Figs. 7A and 7B show induction of IFN-γ from a human anti-*chlamydia* T-eell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* upon activation by monocyte-derived dendritic cells expressing chlamydial proteins.

Fig. 8 shows the identification of T cell epitopes in Chlamydial ribosomal S13 protein with T-cell line TCL 8 EB/DC.

Fig. 9A and B illustrate the proliferative response of CP-21 T-cells generated against *C. pnuemoniae*-infected dendritic cells to recombinant *C. pneumonia*-SWIB protein, but not *C. trachomatis* SWIB protein.

Fig. 10 shows the *C. trachomatis*-specific SWIB proliferative responses of a primary T-cell line (TCT-10 EB) from an asymptomatic donor.

Fig. 11 illustrates the identification of T-cell epitope in *C. trachomatis* SWIB with an antigen specific T-cell line (TCL-10 EB).

Fig. 12 shows the *C. trachomatis*-specific proliferative responses of primary T cell lines generated from two patients against the CT specific antigens CT622, CT875 and CT EB.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis and treatment of Chlamydial infection. In one aspect, the compositions of the subject invention include polypeptides that comprise at least one immunogenic portion of a *Chlamydia* antigen, or a variant thereof.

In specific embodiments, the subject invention discloses polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, wherein the *Chlamydia* antigen comprises an amino acid sequence encoded by a polynucleotide molecule disclosed herein, the complements of said nucleotide sequences, and variants of such sequences.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the inventive antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences

may be derived from the native *Chlamydia* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

The term “polynucleotide(s),” as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of “polynucleotide” therefore includes all such operable anti-sense fragments.

An "immunogenic portion" of an antigen is a portion that is capable of reacting with sera obtained from a *Chlamydia*-infected individual (*i.e.*, generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a representative ELISA assay described herein). Such immunogenic portions generally comprise at least about 5 amino acid residues, more preferably at least about 10, and most preferably at least about 20 amino acid residues. Methods for preparing and identifying immunogenic portions of antigens of known sequence are well known in the art and include those summarized in Paul, *Fundamental Immunology*, 3rd ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.,* they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native *Chlamydia* protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.,* in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is

similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual,* Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ^{125}I-labeled Protein A.

Examples of immunogenic portions of antigens contemplated by the present invention include, for example, the T cell stimulating epitopes provided in SEQ ID NO: 9, 10, 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256. Polypeptides comprising at least an immunogenic portion of one or more *Chlamydia* antigens as described herein may generally be used, alone or in combination, to detect Chlamydial infection in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotide molecules. Such variants include, but are not limited to, naturally occurring allelic variants of the inventive sequences. In particular, variants include other *Chlamydiae* serovars, such as serovars D, E and F, as well as the several LGV serovars which share homology to the inventive polypeptide and polynucleotide molecules described herein. Preferably, the serovar homologues show 95-99% homology to the corresponding polypeptide sequence(s) described herein.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above

polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.,* 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide. Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to

enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A polynucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions such that the immunogenicity of the encoded polypeptide is not diminished, relative to the native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA, 2*:183, 1983). Nucleotide variants may be naturally occurring allelic variants as discussed below, or non-naturally occurring variants. The polypeptides provided by the present invention include variants that are encoded by polynucleotide sequences which are substantially homologous to one or more of the polynucleotide sequences specifically recited herein. "Substantial homology," as used herein, refers to polynucleotide sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing polynucleotide sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode a polypeptide that is the same as a polypeptide of the present invention.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Resarch Foundaiton, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenes pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS 5*:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS 4*:11-17; Robinson, E.D. (1971) *Comb. Theor 11*:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol. 4*:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA 80*:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity methods of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. (U.S.A.) 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One illustrative example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul et al. (1990) J. Mol. Biol. 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for

Biotechnology Information (http://www.ncbi.nlm.nih.gov/) In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or amino acid sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention provides polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% or more sequence identity, preferably at least 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (e.g., BLAST analyisis using standard parameters, as described below). One skilled in this art will recognize that these values can be

appropriately adjusted to determine corresponding identity of proteins encoded by two polynucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides or polypeptides comprising various lengths of contiguous stretches of sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides and polypeptides encompassed by this invention may comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the disclosed sequences, as well as all intermediate lengths therebetween. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through the 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

Also included in the scope of the present invention are alleles of the genes encoding the nucleotide sequences recited in herein. As used herein, an "allele" or "allellic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of

nucleotides. Each of these types of changes may occur alone or in combination with the others, one or more times in a given sequence.

In specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *Chlamydia* antigen (or a variant of such an antigen), that comprises one or more of the amino acid sequences encoded by (a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 358-361, 407-430, 525-559, 582-598; (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b). As discussed in the Examples below, several of the *Chlamydia* antigens disclosed herein recognize a T cell line that recognizes both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, indicating that they may represent an immunoreactive epitope shared by *Chlamydia trachomatis* and *Chlamydia pneumoniae.* The antigens may thus be employed in a vaccine for both *C. trachomatis* genital tract infections and for *C. pneumonia* infections. Further characterization of these *Chlamydia* antigens from *Chlamydia trachomatis* and *Chlamydia pneumonia* to determine the extent of eross-reactivity is provided in Example 6. Additionally, Example 4 describes cDNA fragments (SEQ ID NO: 15, 16 and 33) isolated from *C. trachomatis* which encode proteins (SEQ ID NO: 17-19 and 32) capable of stimulating a *Chlamydia*-specific murine CD8+ T cell line.

In general, *Chlamydia* antigens, and polynucleotide sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, polynucleotide molecules encoding *Chlamydia* antigens may be isolated from a *Chlamydia* genomic or cDNA expression library by screening with a *Chlamydia*-specific T eell line as described below, and sequenced using techniques well known to those of skill in the art. Additionally, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for *Chlamydia*-associated expression (*i.e.,* expression that is at least two fold greater in *Chlamydia*-infected cells than in controls, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as deseribed by Schena et al., *Proc. Natl. Acad. Sci. USA 93*:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA 94*:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA

prepared from cells expressing the proteins described herein.. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purehased or synthesized.

Antigens may be produced recombinantly, as described below, by inserting a polynucleotide sequence that encodes the antigen into an expression vector and expressing the antigen in an appropriate host. Antigens may be evaluated for a desired property, such as the ability to react with sera obtained from a *Chlamydia*-infected individual as described herein, and may be sequeneed using, for example, traditional Edman chemistry. *See* Edman and Berg, *Eur. J. Biochem. 80*:116-132, 1967.

Polynucleotide sequences encoding antigens may also be obtained by screening an appropriate *Chlamydia* cDNA or genomic DNA library for polynucleotide sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic aeid probe from a cDNA or genomic library. The library screen may then be performed using the isolated probe.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.,* a *Chlamydia* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.,* by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see*

Sambrook et al., *Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using techniques well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol. 51*:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989), and software well known in the art may also be employed. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as deseribed above, and overlapping sequences assembled into a eontiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res. 16*:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods*

Applic. 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Transcription-Mediated Amplification, or TMA is another method that may be utilized for the amplification of DNA, rRNA, or mRNA, as described in Patent No. PCT/US91/03184. This autocatalytic and isothermic non-PCR based method utilizes two primers and two enzymes: RNA polymerase and reverse transcriptase. One primer contains a promoter sequence for RNA polymerase. In the first amplification, the promoter-primer hybridizes to the target rRNA at a defined site. Reverse transcriptase creates a DNA copy of the target rRNA by extension from the 3'end of the promoter-primer. The RNA in the resulting complex is degraded and a second primer binds to the DNA copy. A new strand of DNA is synthesized from the end of the primer by reverse transcriptase creating double stranded DNA. RNA polymerase recognizes the promoter sequence in the DNA template and initiates transcription. Each of the newly synthesized RNA amplicons re-enters the TMA process and serves as a template for a new round of replication leading to the expotential expansion of the RNA amplicon. Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length cDNA sequences may also be obtained by analysis of genomic fragments.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA 2*:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a *Chlamydial* protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded

polypeptide is generated *in vivo* (*e.g.,* by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a *Chlamydial* polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.,* an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transeribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a *Chlamydial* protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.,* promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of

particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc. 85*:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

As noted above, immunogenic portions of *Chlamydia* antigens may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative ELISAs described herein may generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of a *Chlamydia* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model ELISA as described herein.

Portions and other variants of *Chlamydia* antigens may be generated by synthetic or recombinant means. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a polynucleotide sequence encoding the

polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the coneentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a reeombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides as described herein. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host eells inelude prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure.

Within certain speeific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known *Chlamydial* protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein. A DNA sequence encoding a fusion protein of the present invention may be constructed using known recombinant

DNA techniques to assemble separate DNA sequences encoding, for example, the first and second polypeptides, into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with funetional epitopes on the first and second polypeptides; and (3) the lack of hydrophobie or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene 40*:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA 83*:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino aeids in length. As an alternative to the use of a peptide linker sequence (when desired), one can utilize non-essential N-terminal amino acid regions (when present) on the first and second polypeptides to separate the functional domains and prevent sterie hindrance.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the

immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, *336*:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium Haemophilus influenza B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemaglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene 43*:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10*:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In another embodiment, a Mycobacterium tuberculosis-derived Ra12 polynucleotide is linked to at least an immunogenic portion of a polynucleotide of this invention. Ra12 compositions and methods for their use inenhancing expression of heterologous polynucleotide sequences is described in U.S. Patent Application

60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (U.S. Patent Application 60/158,585; see also, Skeiky *et al.*, *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference. In one embodiment, the Ra12 polypeptide used in the production of fusion polypeptides comprises a C-terminal fragment of the MTB32A coding sequence that is effective for enhancing the expression and/or immunogenicity of heterologous Chlamydial antigenic polypeptides with which it is fused. In another embodiment, the Ra12 polypeptide corresponds to an approximately 14 kD C-terminal fragment of MTB32A comprising some or all of amino acid residues 192 to 323 of MTB32A.

Recombinant nucleic acids, which encode a fusion polypeptide comprising a Ra12 polypeptide and a heterologous Chlamydia polypeptide of interest, can be readily constructed by conventional genetic engineering techniques. Recombinant nucleic acids are constructed so that, preferably, a Ra12 polynucleotide sequence is located 5' to a selected heterologous Chlamydia polynucleotide sequenee. It may also be appropriate to place a Ra12 polynucleotide sequence 3' to a selected heterologous polynucleotide sequence or to insert a heterologous polynucleotide sequence into a site within a Ra12 polynucleotide sequence.

In addition, any suitable polynucleotide that encodes a Ra12 or a portion or other variant thereof can be used in constructing recombinant fusion polynucleotides comprising Ra12 and one or more Chlamydia polynucleotides disclosed herein. Preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide.

Ra12 polynucleotides may comprise a native sequence (*i.e.,* an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one

or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against Chlamydial infection in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat Chlamydial infection.

In this aspect, the polypeptide, fusion protein or polynucleotide molecule is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and an immunostimulant, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *Chlamydia* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain polynucleotides encoding one or more polypeptides or fusion proteins as described above, such that the polypeptide is generated *in situ*. In such vaccines, the polynucleotides may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary polynucleotide sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a

preferred embodiment, the polynucleotides may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective) virus. Techniques for incorporating polynucleotides into such expression systems are well known to those of ordinary skill in the art. The polynucleotides may also be administered as "naked" plasmid vectors as described, for example, in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993.Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.,* an artificial membrane vesicle). The uptake of naked polynucleotides may be increased by incorporating the polynucleotides into and/or onto biodegradable beads, which are efficiently transported into the cells. The preparation and use of such systems is well known in the art.

In a related aspect, a polynucleotide vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *Chlamydia* antigen. For example, administration of polynucleotides encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Polypeptides and polynucleotides disclosed herein may also be employed in adoptive immunotherapy for the treatment of *Chlamydial* infection. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous

host immune system with the administration of immune response-modifying agents (for example, vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate anti-*Chlamydia* effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper), killer cells (such as Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast, or B-cells, may be pulsed with immunoreactive polypeptides, or polynucleotide sequence(s) may be introduced into antigen presenting cells, using a variety of standard techniques well known in the art. For example, antigen presenting cells may be transfected or transduced with a polynucleotide sequence, wherein said sequence contains a promoter region appropriate for increasing expression, and can be expressed as part of a recombinant virus or other expression system. Several viral vectors may be used to transduce an antigen presenting cell, including pox virus, vaccinia virus, and adenovirus; also, antigen presenting cells may be transfected with polynucleotide sequences disclosed herein by a variety of means, including gene-gun technology, lipid-mediated delivery, electroporation, osmotic shock, and particlate delivery mechanisms, resulting in efficient and acceptable expression levels as determined by one of ordinary skill in the art. For cultured T-cells to be effective in

therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever, M., *et al*, "Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews, 157*:177, 1997).

The polypeptides disclosed herein may also be employed to generate and/or isolate chlamydial-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed polypeptides. The resulting antigen specific CD8+ or CD4+ T-cell clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate *Chlamydia* reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by Chang *et al, (Crit. Rev. Oncol. Hematol., 22*(3), 213, 1996). Cells of the immune system, sueh as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as Isolex™ System, available from Nexell Therapeutics, Inc. Irvine, CA. The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

In other embodiments, T-eell and/or antibody receptors specific for the polypeptides disclosed herein can be cloned, expanded, and transferred into other vectors or effector cells for use in adoptive immunotherapy. In particular, T cells may be transfected with the appropriate genes to express the variable domains from chlamydia specific monoclonal antibodies as the extracellular recognition elements and joined to the T cell receptor signaling chains, resulting in T cell activation, specific lysis, and cytokine release. This enables the T cell to redirect its specificity in an MHC-independent manner. See for example, Eshhar, Z., *Cancer Immunol Immunother*, 45(3-

4):131-6, 1997 and Hwu, P., et al, *Cancer Res*, 55(15):3369-73, 1995. Another embodiment may include the transfection of chlamydia antigen spccific alpha and beta T cell receptor chains into alternate T cells, as in Cole, DJ, et al, *Cancer Res*, 55(4):748-52, 1995.

In a further embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generatc antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate discase in a murine model has been demonstrated by Cheever ct al, *Immunological Reviews, 157*:177, 1997). Additionally, vectors expressing the disclosed polynucleotides may bc introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.,* vaccines). Alternatively, a pharmaceutical composition may comprise an antigen-presenting cell (*e.g.* a dendritic cell) transfected with a *Chlamydial* polynucleotide such that the antigen presenting cell expresses a *Chlamydial* polypeptide. Pharmaceutical compositions eomprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may bc any substance that enhances or potentiates an immune responsc to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.,* polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.,* Fullerton, U.S. Patent No. 4,235,877). Vaccine prcparation is generally describcd in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invcntion may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of othcr *Chlamydial* antigens may bc present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems 15*:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.,* vaccinia or other pox virus, retrovirus, adenovirus, baculovirus, togavirus, bacteriophage, and the like), which often involves the use of a non-pathogenic (defective), replication competent virus.

For example, many viral expression vectors are derived from viruses of the retroviridae family. This family includes the murine leukemia viruses, the mouse mammary tumor viruses, the human foamy viruses, Rous sarcoma virus, and the immunodeficiency viruses, including human, simian, and feline. Considerations when designing retroviral expression vectors are discussed in Comstock *et al.* (1997).

Excellent murine leukemia virus (MLV)-based viral expression vectors have been developed by Kim *et al.* (1998). In creating the MLV vectors, Kim *et al.* found that the entire *gag* sequence, together with the immediate upstream region, could be deleted without significantly affecting viral packaging or gene expression. Further, it was found that nearly the entire U3 region could be replaced with the immediately-early promoter of human cytomegalovirus without deleterious effects. Additionally, MCR and internal ribosome entry sites (IRES) could be added without adverse effects. Based on their observations, Kim *et al.* have designed a series of MLV-based expression vectors comprising one or more of the features described above.

As more has been learned about human foamy virus (HFV), characteristics of HFV that are favorable for its use as an expression vector have been

discovered. These characteristics include the expression of pol by splicing and start of translation at a defined initiation codon. Other aspects of HFV viral expression vectors are reviewed in Bodem *et al.* (1997).

Murakami *et al.* (1997) describe a Rous sarcoma virus (RSV)-based replication-competent avian retrovirus vectors, IR1 and IR2 to express a heterologous gene at a high level. In these vectors, the IRES derived from encephalomyocarditis virus (EMCV) was inserted between the *env* gene and the heterologous gene. The IR1 vector retains the splice-acceptor site that is present downstream of the *env* gene while the IR2 vector lacks it. Murakami *et al.* have shown high level expression of several different heterologous genes by these vectors.

Recently, a number of lentivirus-based retroviral expression vectors have been developed. Kafri *et al.* (1997) have shown sustained expression of genes delivered directly into liver and muscle by a human immunodeficiency virus (HIV)-based expression vector. One benefit of the system is the inherent ability of HIV to transduce non-dividing cells. Because the viruses of Kafri *et al.* are pseudotyped with vesicular stomatitis virus G glycoprotein (VSVG), they can transduce a broad range of tissues and cell types.

A large number of adenovirus-based expression vectors have been developed, primarily due to the advantages offered by these vectors in gene therapy applications. Adenovirus expression vectors and methods of using such vectors are the subject of a number of United States patents, including United States Patent No. 5,698,202, United States Patent No. 5,616,326, United States Patent No. 5,585,362, and United States Patent No. 5,518,913, all incorporated herein by reference.

Additional adenoviral constructs are described in Khatri *et al.* (1997) and Tomanin *et al.* (1997). Khatri *et al.* describe novel ovine adenovirus expression vectors and their ability to infect bovine nasal turbinate and rabbit kidney cells as well as a range of human cell type, including lung and foreskin fibroblasts as well as liver, prostate, breast, colon and retinal lines. Tomanin *et al.* describe adenoviral expression vectors containing the T7 RNA polymerase gene. When introduced into cells containing a heterologous gene operably linked to a T7 promoter, the vectors were able to drive gene expression from the T7 promoter. The authors suggest that this system may be useful for the cloning and expression of genes encoding cytotoxic proteins.

Poxviruses are widely used for the expression of heterologous genes in mammalian cells. Over the years, the vectors have been improved to allow high expression of the heterologous gene and simplify the integration of multiple heterologous genes into a single molecule. In an effort to diminish cytopathic effects and to increase safety, vaccinia virus mutant and other poxviruses that undergo abortive infection in mammalian cells are receiving special attention (Oertli *et al.,* 1997). The use of poxviruses as expression vectors is reviewed in Carroll and Moss (1997).

Togaviral expression vectors, which includes alphaviral expression vectors have been used to study the structure and function of proteins and for protein production purposes. Attractive features of togaviral expression vectors are rapid and efficient gene expression, wide host range, and RNA genomes (Huang, 1996). Also, recombinant vaccines based on alphaviral expression vectors have been shown to induce a strong humoral and cellular immune response with good immunological memory and protective effects (Tubulekas *et al.,* 1997). Alphaviral expression vectors and their use are discussed, for example, in Lundstrom (1997).

In one study, Li and Garoff (1996) used Semliki Forest virus (SFV) expression vectors to express retroviral genes and to produce retroviral particles in BHK-21 cells. The particles produced by this method had protease and reverse transcriptase activity and were infectious. Furthermore, no helper virus could be detected in the virus stocks. Therefore, this system has features that are attractive for its use in gene therapy protocols.

Baculoviral expression vectors have traditionally been used to express heterologous proteins in insect cells. Examples of proteins include mammalian chemokine receptors (Wang *et al.,* 1997), reporter proteins such as green fluorescent protein (Wu *et al.,* 1997), and FLAG fusion proteins (Wu *et al.,* 1997; Koh *et al.,* 1997). Recent advances in baculoviral expression vector technology, including their use in virion display vectors and expression in mammalian cells is reviewed by Possee (1997). Other reviews on baculoviral expression vectors include Jones and Morikawa (1996) and O'Reilly (1997).

Other suitable viral expression systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA 86*:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci. 569*:86-103, 1989; Flexner et al., *Vaccine 8*:17-21, 1990; U.S. Patent

Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques 6*:616-627, 1988; Rosenfeld et al., *Science 252*:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA 91*:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA 90*:11498-11502, 1993; Guzman et al., *Circulation 88*:2838-2848, 1993; and Guzman et al., *Cir. Res. 73*:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. In other systems, the DNA may be introduced as "naked" DNA, as described, for example, in Ulmer et al., *Science 259*:1745-1749, 1993 and reviewed by Cohen, *Science 259*:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

It will be apparent that a vaccine may comprise a polynucleotide and/or a polypeptide component, as desired. It will also be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and/or polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.,* salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.,* sodium, potassium, lithium, ammonium, calcium and magnesium salts).While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, stareh, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.,* polylactate polyglycolate) may also be employed as earriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (*e.g.,* neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.,* glucose, mannose, sucrose or

dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, under select circumstances, the adjuvant composition may be designed to induce an immune response predominantly of the Th1 type or Th2 type. High levels of Th1-type cytokines (*e.g.,* IFN-γ, TNFα, IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type eytokines (*e.g.,* IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science 273*:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.,* SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa Corporation; Seattle, WA), RC-529 (Corixa Corporation; Seattle, WA) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.,* a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g.,* Coombes et al., *Vaccine 14*:1429-1438, 1996) and

administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers inelude supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.,* a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.,* U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the eondition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical eompositions and vaccines to facilitate production of an antigen-specific immune response that targets *Chlamydia*-infeeted cells. Delivery vehieles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-*Chlamydia* effects *per se* and/or to be immunologically compatible with the receiver (*i.e.,* matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature 392*:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic immunity (*see* Timmerman and Levy, *Ann. Rev. Med. 50*:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with

marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med. 4*:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNFα to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNFα, CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fcγ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.,* CD54 and CD11) and costimulatory molecules (*e.g.,* CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a *Chlamydial* protein (or portion or other variant thereof) such that the *Chlamydial* polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein.

Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritie cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritie cells may be achieved by incubating dendritic cells or progenitor cells with the *Chlamydial* polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.,* vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.,* a carrier moleeule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Routes and frequency of administration of pharmaceutical compositions and vaccines, as well as dosage, will vary from individual to individual. In general, the pharmaceutieal eompositions and vaceines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaceinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as deseribed above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *Chlamydial* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injeetion, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid earrier,

such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a *Chlamydial* protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose Chlamydial infection. In this aspect, methods are provided for detecting Chlamydial infection in a biological sample, using one or more of the above polypeptides, either alone or in combination. For clarity, the term "polypeptide" will be used when describing specific embodiments of the inventive diagnostic methods. However, it will be clear to one of skill in the art that the fusion proteins of the present invention may also be employed in such methods.

As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient. The polypeptides are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to *Chlamydia* antigens which may be indicative of *Chlamydia*-infection.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (*i.e.*, one component polypeptide will tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by

using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *Chlamydia*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested.

A variety of assay formats are known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. *See*, *e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (*e.g.*, in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate, or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. In

such eases, adsorption may be achieved by contaeting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contaet time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1 μg, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reaeting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin (BSA) or Tween 20™ (Sigma Chemical Co., St. Louis, MO) may be employed. The immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable dilutent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of antibody within an HGE-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at

equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. Detection reagent may then be added to the solid support. An appropriate detection reagent is any compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of binding agent to reporter group may be aehieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (*e.g.*, Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from thc manufaeturcr's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*Chlamydia* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid

support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for *Chlamydia*-infection. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for Chlamydial infection.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*Chlamydia* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide

immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1 μg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (*e.g.*, one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use with the polypeptides of the present invention. The above descriptions are intended to be exemplary only. One example of an alternative assay protocol which may be usefully employed in such methods is a Western blot, wherein the proteins present in a biological sample are separated on a gel, prior to exposure to a binding agent. Such techniques are well known to those of skill in the art.

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a *Chlamydial* protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a *Chlamydial* protein if it reacts at a detectable level (within, for example, an ELISA) with a *Chlamydial* protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a *Chlamydial* infection using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a *Chlamydial* protein will generate a signal indicating the presence of a *Chlamydial* infection in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without infection. To determine whether a binding agent satisfies this requirement, biological

samples (*e.g.,* blood, sera, sputum urine and/or tissue biopsies) from patients with and without *Chlamydial* infection (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.,* mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol. 6*:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may

be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y, ^{123}I, ^{125}I, ^{131}I, ^{186}Re, ^{188}Re, ^{211}At, and ^{212}Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diptheria

toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reaeting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemieal reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in site-specific regions by appropriate methods. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density, and the rate of clearance of the antibody.

Antibodies may be used in diagnostic tests to detect the presence of *Chlamydia* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting Chlamydial infection in a patient.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a

polymerase chain reaction (PCR) based assay to amplify *Chlamydia*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *Chlamydia*-specific sequences in biological samples. DNA probes or primers comprising oligonucleotide sequences described above may be used alone or in combination with each other.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

ISOLATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS

Chlamydia antigens of the present invention were isolated by expression cloning of a genomic DNA library of *Chlamydia trachomatis* LGV II essentially as described by Sanderson et al. (*J. Exp. Med.*, 1995, *182*:1751-1757) and were shown to induce PBMC proliferation and IFN-γ in an immunoreactive T cell line.

A *Chlamydia*-specific T cell line was generated by stimulating PBMCs from a normal donor with no history of chlamydial genital tract infection with elementary bodies of *Chlamydia trachomatis* LGV II. This T cell line, referred to as TCL-8, was found to recognize both *Chlamydia trachomatis* and *Chlamydia pneumonia* infected monocyte-derived dendritic cells.

A randomly sheared genomic library of *Chlamydia trachomatis* LGV II was constructed in Lambda ZAP (Stratagene, La Jolla, CA) and the amplified library plated out in 96 well microtiter plates at a density of 30 clones/well. Bacteria were induced to express recombinant protein in the presence of 2 mM IPTG for 3 h, then pelleted and resuspended in 200 μl of RPMI 10% FBS. 10 μl of the induced bacterial suspension was transferred to 96 well plates containing autologous monocyte-derived dendritic cells. After a 2 h incubation, dendritie cells were washed to remove free *E. coli* and *Chlamydia*-specific T cells were added. Positive *E. coli* pools were identified by determining IFN-γ production and proliferation of the T cells in response to the pools.

Four positive pools were identified, which were broken down to yield four pure clones (referred to as 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31), with insert sizes of 481 bp, 183 bp, 110 bp and 1400 bp, respectively. The determined DNA sequences for 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31 are provided in SEQ ID NO: 1-4, respectively. Clone 1-B1-66 is approximately in region 536690 of the *C. trachomatis* genome (NCBI *C. trachomatis* database). Within clone 1-B1-66, an open reading frame (ORF) has been identified (nucleotides 115 - 375) that encodes a previously identified 9 kDa protein (Stephens, et al. Genbank Accession No. AE001320), the sequence of which is provided in SEQ ID NO: 5). Clone 4-D7-28 is a smaller region of the same ORF (amino acids 22-82 of 1-B1-66). Clone 3-G3-10 is approximately in region 74559 of the *C. trachomatis* genome. The insert is cloned in the antisense orientation with respect to its orientation in the genome. The clone 10-C10-31 contains an open reading frame that corresponds to a previously published sequence for S13 ribosomal protein from *Chlamydia trachomatis* (Gu, L. et al. *J. Bacteriology*, *177*:2594-2601, 1995). The predicted protein sequences for 4-D7-28 and 10-C10-31 are provided in SEQ ID NO: 6 and 12, respectively. Predicted protein sequences for 3-G3-10 are provided in SEQ ID NO: 7-11.

In a related series of screening studies, an additional T cell line was used to screen the genomic DNA library of *Chlamydia trachomatis* LGV II described above. A *Chlamydia*-specific T cell line (TCT-1) was derived from a patient with a chlamydial genital tract infection by stimulating patient PBMC with autologous monocyte-derived dendritic cells infeeted with elementary bodies of *Chlamydia trachomatis* LGV II. One clone, 4C9-18 (SEQ ID NO: 21), containing a 1256 bp insert, elicited a specific immune response, as measured by standard proliferation assays, from the *Chlamydia*-specific T eell line TCT-1. Subsequent analysis revealed this clone to contain three known sequences: lipoamide dehydrogenase (Genbank Accession No. AE001326), disclosed in SEQ ID NO: 22; a hypothetical protein CT429 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 23; and part of an open reading frame of ubiquinone methyltransferase CT428 (Genbank Aecession No. AE001316), disclosed in SEQ ID NO: 24.

In further studies involving clone 4C9-18 (SEQ ID NO: 21), the full-length amino acid sequence for lipoamide dehydrognase (SEQ ID NO: 22) from *C. trachomatis* (LGV II) was expressed in elone CtL2-LPDA-FL, as disclosed in SEQ ID NO: 90.

To further characterize the open reading frame containing the T cell stimulating epitope(s), a cDNA fragment containing nucleotides 1-695 of clone 4C9-18 with a cDNA sequenee encoding a 6X-Histidine tag on the amino terminus was subcloned into the NdeI/EcoRI site of the pET17b vector (Novagen, Madison, WI), referred to as clone 4C9-18#2 BL21 pLysS (SEQ ID NO: 25, with the eorresponding amino acid sequence provided in SEQ ID NO: 26) and transformed into *E. coli*. Selective induction of the transformed *E. coli* with 2 mM IPTG for three hours resulted in the expression of a 26 kDa protein from clone 4C9-18#2 BL21 pLysS, as evidenced by standard Coomassie-stained SDS-PAGE. To determine the immunogenicity of the protein encoded by clone 4C9-18#2 BL21 pLysS, *E. coli* expressing the 26 kDa protein were titered onto 1 x 10^4 monoeyte-derived dendritic cells and incubated for two hours. The dendritic cell cultures were washed and 2.5 x 10^4 T cells (TCT-1) added and allowed to incubate for an additional 72 hours, at which time the level of IFN-γ in the culture supernatant was determined by ELISA. As shown in Fig. 1, the T-cell line TCT-1 was found to respond to induced cultures as measured by IFN-g, indicating a

Chlamydia-specific T-cell response against the lipoamide dehydrogenase sequence. Similarly, the protein encoded by clone 4C9-18#2 BL21 pLysS was shown to stimulate the TCT-1 T-cell line by standard proliferation assays.

Subsequent studies to identify additional *Chlamydia trachomatis* antigens using the above-described CD4+ T-cell expression cloning technique yielded additional clones. The TCT-1 and TCL-8 *Chlamydia*-specific T-cell lines, as well as the TCP-21 T-cell line were utilized to screen the *Chlamydia trachomatis* LGVII genomic library. The TCP-21 T-cell line was derived from a patient having a humoral immune response to *Chlamydia pnuemoniae.* The TCT-1 cell line identified 37 positive pools, the TCT-3 cell line identified 41 positive pools and the TCP-21 cell line identified 2 positive pools. The following clones were derived from 10 of these positive pools. Clone 11-A3-93 (SEQ ID NO: 64), identified by the TCP-21 cell line, is a 1339 bp genomic fragment sharing homology to the HAD superfamily (CT103). The second insert in the same clone shares homology with the fab I gene (CT104) present on the complementary strand. Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pnuemoniae*.

Clone 11-G10-46, (SEQ ID NO: 62), identified using the TCT-3 cell line, contains a 688 bp insert that shares homology to the hypothetical protein CT610. Clone 11-G1-34, (SEQ ID NO: 61), identified using the TCT-3 cell line, has two partial open reading frames (ORF) with an insert size of 1215 bp. One ORF shares homology to the malate dehydrogenase gene (CT376), and the other ORF shares homology to the glycogen hydrolase gene (CT042). Clone 11-H3-68, (SEQ ID NO: 60), identified using the TCT-3 cell line, has two ORFs with a total insert size of 1180 bp. One partial ORF encodes the plasmid-encoded PGP6-D virulence protein while the second ORF is a complete ORF for the L1 ribosomal gene (CT318). Clone 11-H4-28, (SEQ ID NO: 59), identified using the TCT-3 cell line, has an insert size of 552 bp and is part of the ORF for the dnaK gene (CT396). Clone 12-B3-95, (SEQ ID NO: 58), identified using the TCT-1 cell line, has an insert size of 463 bp and is a part of the ORF for for the lipoamide dehydrogenase gene (CT557). Clones 15-G1-89 and 12-B3-95 are identical, (SEQ ID NO: 55 and 58, respectively), identified using the TCT-1 cell line, has an insert size of 463 bp and is part of the ORF for the lipoamide dehydrogenase gene

(CT557). Clone 12-G3-83, (SEQ ID NO: 57), identified using the TCT-1 cell line, has an insert size of 1537 bp and has part of the ORF for the hypothetical protein CT622.

Clone 23-G7-68, (SEQ ID NO: 79), identified using the TCT-3 cell line, contains a 950 bp insert and contains a small part of the L11 ribosomal ORF, the entire ORF for L1 ribosomal protein and a part of the ORF for L10 ribosomal protein. In addition, this clone also identified the patient lines CT4, CT5, CT11, CT12, and CHH037. Clone 22-F8-91, (SEQ ID NO: 80), identified using the TCT-1 cell line, contains a 395 bp insert that contains a part of the pmpC ORF on the complementary strand of the clone. Clone 21-E8-95, (SEQ ID NO: 81), identified using the TCT-3 cell line, contains a 2,085 bp insert which contains part of CT613 ORF, the complete ORF for CT612, the complete ORF for CT611 and part of the ORF for CT610. Clone 19-F12-57, (SEQ ID NO: 82), identified using the TCT-3 cell line, contains a 405 bp insert which contains part of the CT 858 ORF and a small part of the recA ORF. Clone 19-F12-53, (SEQ ID NO: 83), identified using the TCT-3 cell line, contains a 379 bp insert that is part of the ORF for CT455 encoding glutamyl tRNA synthetase. Clone 19-A5-54, (SEQ ID NO: 84), identified using the TCT-3 cell line, contains a 715 bp insert that is part of the ORF3 (complementary strand of the clone) of the cryptic plasmid. Clone 17-E11-72, (SEQ ID NO: 85), identified using the TCT-1 cell line, contains a 476 bp insert that is part of the ORF for Opp_2 and pmpD. The pmpD region of this clone is covered by the pmpD region of clone 15-H2-76. Clone 17-C1-77, (SEQ ID NO: 86), identified using the the patient cell lines CT3, CT1, CT4, and CT12, contains a 1551 bp insert that is part of the CT857 ORF, as well as part of the CT858 ORF. Clone 15-H2-76, (SEQ ID NO: 87), identified using the TCT-1 cell line, contains a 3,031 bp insert that contains a large part of the pmpD ORF, part of the CT089 ORF, as well as part of the ORF for SycE. Clone 15-A3-26, (SEQ ID NO: 88), contains a 976 bp insert that contains part of the ORF for CT858. Clone 17-G4-36, (SEQ ID NO: 267), identified using the patient lines CL8, TCT-10, CT1, CT5, CT13, and CHH037, contains a 680 bp insert that is in frame with beta-gal in the plasmid and shares homology to part of the ORF for DNA-directed RNA polymerase beta subunit (CT315 in SerD).

Several of the clones described above share homology to various polymorphic membrane proteins. The genomic sequence of *Chlamydia trachomatis* contains a family of nine polymorphic membrane protein genes, referred to as pmp.

These genes are designated pmpA, pmpB, pmpC, pmpD, pmpE, pmpF, pmpG, pmpH and pmpI. Proteins expressed from these genes are believed to be of biological relevance in generating a protective immune response to a *Chlamydial* infection. In particular, pmpC, pmpD, pmpE and pmpI contain predictable signal peptides, suggesting they are outer membrane proteins, and therefore, potential immunological targets.

Based on the *Chlamydia trachomatis* LGVII serovar sequence, primer pairs were designed to PCR amplify the full-length fragments of pmpC, pmpD, pmpE, pmpG, pmpH and pmpI. The resulting fragments were subcloned into the DNA vaccine vector JA4304 or JAL, which is JA4304 with a modified linker (SmithKline Beecham, London, England). Specifically, PmpC was subcloned into the JAL vector using the 5' oligo GAT AGG CGC GCC GCA ATC ATG AAA TTT ATG TCA GCT ACT GCT G and the 3' oligo CAG AAC GCG TTT AGA ATG TCA TAC GAG CAC CGC A, as provided in SEQ ID NO: 197 and 198, respectively. PCR amplification of the gene under conditions well known in the art and ligation into the 5' ASCI/3' MluI sites of the JAL vector was completed after inserting the short nucleotide sequence GCAATC (SEQ ID NO: 199) upstream of the ATG to create a Kozak-like sequence. The resulting expression vector contained the full-length pmpC gene comprising 5325 nucleotides (SEQ ID NO: 173) containing the hypothetical signal sequence, which encodes a 187 kD protein (SEQ ID NO: 179). The pmpD gene was subcloned into the JA4304 vaccine vector following PCR amplification of the gene using the following oligos: 5' oligo-TGC AAT CAT GAG TTC GCA GAA AGA TAT AAA AAG C (SEQ ID NO: 200) and 3' oligo- CAG AGC TAG CTT AAA AGA TCA ATC GCA ATC CAG TAT TC (SEQ ID NO: 201). The gene was ligated into the a 5' blunted HIII/3' MluI site of the JA4304 vaccine vector using standard techniques well known in the art. The CAATC (SEQ ID NO: 202) was inserted upstream of the ATG to create a Kozak-like sequence. This clone is unique in that the last threonine of the HindIII site is missing due to the blunting procedure, as is the last glycine of the Kozak-like sequence. The insert, a 4593 nucleotide fragment (SEQ ID NO: 172) is the full-length gene for pmpD containing the hypothetical signal sequence, which encodes a 161 kD protein (SEQ ID NO: 178). PmpE was subcloned into the JA4304 vector using the 5' oligo- TGC AAT CAT GAA AAA AGC GTT TTT CTT TTT C (SEQ ID NO: 203), and the 3' oligo- CAG AAC

GCG TCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 204). Following PCR amplification, the gene was ligated into the 5' blunted HIII/3' MluI site of JA4304. To facilitate this, a short nucleotide sequence, TGCAATC (SEQ ID NO: 293), was added upstream of the initiation codon for creating a Kozak-like sequence and reconstituting the HindIII site. The insert is the full-length pmpE gene (SEQ ID NO: 171) containing the hypothetical signal sequence. The pmpE gene encodes a 105 kD protein (SEQ ID NO: 177). The pmpG gene was PCR amplified using the 5' oligo- GTG CAA TCA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 205), and the 3' oligo- CAG AAC GCG TTT AGA ACC GGA CTT TAC TTC C (SEQ ID NO: 206) and subcloned into the JA4304 vector. Similar cloning strategies were followed for the pmpI and pmpK genes. In addition, primer pairs were designed to PCR amplify the full-length or overlapping fragments of the pmp genes, which were then subcloned for protein expression in the pET17b vector (Novagen, Madison, WI) and transfected into E. coli BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Several of the genes encoding the recombinant proteins, as described below, lack the native signal sequence to facilitate expression of the protein. Full-length protein expression of pmpC was accomplished through expression of two overlapping fragments, representing the amino and carboxy termini. Subcloning of the pmpC-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 187, with the corresponding amino acid sequence provided in SEQ ID NO: 195) used the 5' oligo- CAG ACA TAT GCA TCA CCA TCA CCA TCA CGA GGC GAG CTC GAT CCA AGA TC (SEQ ID NO: 207), and the 3' oligo- CAG AGG TAC CTC AGA TAG CAC TCT CTC CTA TTA AAG TAG G (SEQ ID NO: 208) into the 5' NdeI/3' KPN cloning site of the vector. The carboxy terminus portion of the gene, pmpC-carboxy terminal fragment (SEQ ID NO: 186, with the corresponding amino acid sequence provided in SEQ ID NO: 194), was subcloned into the 5' NheI/3' KPN cloning site of the expression vector using the following primers: 5' oligo- CAG AGC TAG CAT GCA TCA CCA TCA CCA TCA CGT TAA GAT TGA GAA CTT CTC TGG C (SEQ ID NO: 209), and 3' oligo- CAG AGG TAC CTT AGA ATG TCA TAC GAG CAC CGC AG (SEQ ID NO: 210). PmpD was also expressed as two overlapping proteins. The pmpD-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 185, with the corresponding amino acid sequence provided in

SEQ ID NO: 193) contains the initiating codon of the pET17b and is expressed as a 80 kD protein. For protein expression and purification purposes, a six-histidine tag follows the initiation codon and is fused at the 28th amino acid (nucleotide 84) of the gene. The following primers were used, 5' oligo, CAG ACA TAT GCA TCA CCA TCA CCA TCA CGG GTT AGC (SEQ ID NO: 211), and the 3' oligo- CAG AGG TAC CTC AGC TCC TCC AGC ACA CTC TCT TC (SEQ ID NO: 212), to splice into the 5' NdeI/3' KPN cloning site of the vector. The pmpD-carboxy terminus portion (SEQ ID NO: 184) was expressed as a 92 kD protein (SEQ ID NO: 192). For expression and subsequent purification, an additional methionine, alanine and serine was included, which represent the initiation codon and the first two amino acids from the pET17b vector. A six-histidine tag downstream of the methionine, alanine and serine is fused at the 691st amino acid (nucleotide 2073) of the gene. The 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CGG TGC TAT TTC TTG CTT ACG TGG (SEQ ID NO: 213) and the 3' oligo- CAG AGG TAC TTn AAA AGA TCA ATC GCA ATC CAG TAT TCG (SEQ ID NO: 214) were used to subclone the insert into the 5' NheI/3' KPN cloning site of the expression vector. PmpE was expressed as a 106kD protein (SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191). The pmpE insert also lacks the native signal sequence. PCR amplification of the gene under conditions well known in the art was performed using the following oligo primers: 5' oligo- CAG AGG ATC CAC ATC ACC ATC ACC ATC ACG GAC TAG CTA GAG AGG TTC (SEQ ID NO: 215), and the 3' oligo- CAG AGA ATT CCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 216), and the amplified insert was ligated into a 5' BamHI/3' EcoRI site of JA4304. The short nucleotide sequence, as provided in SEQ ID NO: 217, was inserted upstream of the initiation codon for creating the Kozak-like sequence and reconstituting the HindIII site. The expressed protein contains the initiation codon and the downstream 21 amino acids from the pET17b expression vector, i.e., MASMTGGQQMGRDSSLVPSSDP (SEQ ID NO: 218). In addition, a six-histidine tag is included upstream of the sequence described above and is fused at the 28th amino acid (nucleotide 84) of the gene, which eliminates the hypothetical signal peptide. The sequences provided in SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191 do not include these additional sequences. The pmpG gene (SEQ ID NO: 182, with the corresponding

amino acid sequence provided in SEQ ID No; 190) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGG TAC CGC ATC ACC ATC ACC ATC ACA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 219), and the 3' oligo- CAG AGC GGC CGC TTA GAA CCG GAC TTT ACT TCC (SEQ ID NO: 220), and ligated into the 5' KPN/3' NotI cloning site of the expression vector. The expressed protein contains an additional amino acid sequence at the amino end, namely, MASMTGGQQNGRDSSLVPHHHHHH (SEQ ID NO: 221), which comprises the initiation codon and additional sequence from the pET17b expression vector. The pmpI gene (SEQ ID NO: 181, with the corresponding amino acid sequence provided in SEQ ID No; 189) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CCT CTT TGG CCA GGA TCC C (SEQ ID NO: 222), and the 3' oligo- CAG AAC TAG TCT AGA ACC TGT AAG TGG TCC (SEQ ID NO: 223), and ligted into the expression vector at the 5' NheI/3' SpeI cloning site. The 95 kD expressed protein contains the initiation codon plus an additional alanine and serine from the pET17b vector at the amino end of the protein. In addition, a six-histidine tag is fused at the 21st amino acid of the gene, which eliminates the hypothetical signal peptide.

Clone 14H1-4, (SEQ ID NO: 56), identified using the TCT-3 cell line, contains a complete ORF for the TSA gene, thiol specific antioxidant – CT603 (the CT603 ORF is a homolog of CPn0778 from *C. pnuemoniae*). The TSA open reading frame in clone 14-H1-4 was amplified such that the expressed protein possess an additional methionine and a 6x histidine tag (amino terminal end). This amplified insert was sub-cloned into the Nde/EcoRI sites of the pET17b vector. Upon induction of this clone with IPTG, a 22.6 kDa protein was purified by Ni-NTA agarose affinity chromatography. The determined amino acid sequence for the 195 amino acid ORF of clone 14-H1-4 encoding the TSA gene is provided in SEQ ID NO: 65. Further analysis yielded a full-length clone for the TSA gene, referred to as CTL2-TSA-FL, with the full-length amino acid sequence provided in SEQ ID NO: 92.

Further studies yielded 10 additional clones identified by the TCT-1 and TCT-3 T-cell lines, as described above. The clones identified by the TCT-1 line are: 16-D4-22, 17-C5-19, 18-C5-2, 20-G3-45 and 21-C7-66; clones identified by the TCT-3

cell line are: 17-C10-31, 17-E2-9, 22-A1-49 and 22-B3-53. Clone 21-G12-60 was recognized by both the TCT-1 and TCT-3 T cell lines. In addition, clone 20-G3-45, which contained sequence specific for pmpB, was identified against the patient lines CT1 and CT4. Clone 16-D4-22 (SEQ ID NO: 119), identified using the TCT-1 cell line contains a 953 bp insert that contains two genes, parts of open reading frame 3 (ORF3) and ORF4 of the *C. trachomatis* plasmid for growth within mammalian cells. Clone 17-C5-19 (SEQ ID NO: 118), contains a 951 bp insert that contains part of the ORF for DT431, encoding for clpP_1 protease and part of the ORF for CT430 (diaminopimelate epimerase). Clone 18-C5-2 (SEQ ID NO: 117) is part of the ORF for S1 ribosomal protein with a 446 bp insert that was identified using the TCT-1 cell line. Clone 20-G3-45 (SEQ ID NO: 116), identified by the TCT-1 cell line, contains a 437 bp insert that is part of the pmpB gene (CT413). Clone 21-C7-8 (SEQ ID NO: 115), identified by the TCT-1 line, contains a 995bp insert that encodes part of the dnaK like protein. The insert of this clone does not overlap with the insert of the TCT-3 clone 11-H4-28 (SEQ ID NO: 59), which was shown to be part of the dnaK gene CT396. Clone 17-C10-31 (SEQ ID NO: 114), identified by the TCT-3 cell line, contains a 976 bp insert. This clone contains part of the ORF for CT858, a protease containing IRBP and DHR domains. Clone 17-E2-9 (SEQ ID NO: 113) contains part of ORFs for two genes, CT611 and CT610, that span a 1142 bp insert. Clone 22-A1-49 (SEQ ID NO: 112), identified using the TCT-3 line, also contains two genes in a 698 bp insert. Part of the ORF for CT660 (DNA gyrase{gyrA_2}) is present on the top strand where as the complete ORF for a hypothetical protein CT659 is present on the complementary strand. Clone 22-B3-53 (SEQ ID NO: 111), identified by the TCT-1 line, has a 267 bp insert that encodes part of the ORF for GroEL (CT110). Clone 21-G12-60 (SEQ ID NO: 110), identified by both the TCT-1 and TCT-3 cell lines contains a 1461 bp insert that contains partial ORFs for hypothetical proteins CT875, CT229 and CT228.

Additional *Chlamydia* antigens were obtained by screening a genomic expression library of *Chlamydia trachomatis* (LGV II serovar) in Lambda Screen-1 vector (Novagen, Madison, WI) with sera pooled from several *Chlamydia*-infected individuals using techniques well known in the art. The following immuno-reactive clones were identified and the inserts containing *Chlamydia* genes sequenced: CTL2#1 (SEQ ID NO: 71); CTL2#2 (SEQ ID NO: 70); CTL2#3-5' (SEQ ID NO: 72, a first

determined genomic sequence representing the 5' end); CTL2#3-3' (SEQ ID NO: 73, a second determined genomic sequence representing the 3' end); CTL2#4 (SEQ ID NO: 53); CTL2#5 (SEQ ID NO: 69); CTL2#6 (SEQ ID NO: 68); CTL2#7 (SEQ ID NO: 67); CTL2#8b (SEQ ID NO: 54); CTL2#9 (SEQ ID NO: 66); CTL2#10-5' (SEQ ID NO: 74, a first determined genomic sequence representing the 5' end); CTL2#10-3' (SEQ ID NO: 75, a second determined genomic sequence representing the 3' end); CTL2#11-5' (SEQ ID NO: 45, a first determined genomic sequence representing the 5' end); CTL2#11-3' (SEQ ID NO: 44, a second determined genomic sequence representing the 3' end); CTL2#12 (SEQ ID NO: 46); CTL2#16-5' (SEQ ID NO: 47); CTL2#18-5' (SEQ ID NO: 49, a first determined genomic sequence representing the 5' end); CTL2#18-3' (SEQ ID NO: 48, a second determined genomic sequence representing the 3' end); CTL2#19-5' (SEQ ID NO: 76, the determined genomic sequence representing the 5' end); CTL2#21 (SEQ ID NO: 50); CTL2#23 (SEQ ID NO: 51; and CTL2#24 (SEQ ID NO: 52).

Additional *Chlamydia trachomatis* antigens were identified by serological expression cloning. These studies used sera pooled from several *Chlamydia*-infected individuals, as described above, but, IgA,and IgM antibodies were used in addition to IgG as a secondary antibody. Clones screened by this method enhance detection of antigens recognized by an early immune response to a *Chlamydial* infection, that is a mucosal humoral immune response. The following immunoreactive clones were characterized and the inserts containing *Chlamydia* genes sequenced: CTL2gam-1 (SEQ ID NO: 290), CTL2gam-2 (SEQ ID NO: 289), CTL2gam-5 (SEQ ID NO: 288), CTL2gam-6-3' (SEQ ID NO: 287, a second determined genomic sequence representing the 3' end), CTL2gam-6-5' (SEQ ID NO: 286, a first determined genomic sequence representing the 5' end), CTL2gam-8 (SEQ ID NO: 285), CTL2gam-10 (SEQ ID NO: 284), CTL2gam-13 (SEQ ID NO: 283), CTL2gam-15-3' (SEQ ID NO: 282, a second determined genomic sequence representing the 3' end), CTL2gam-15-5' (SEQ ID NO: 281, a first determined genomic sequence representing the 5' end), CTL2gam-17 (SEQ ID NO: 280), CTL2gam-18 (SEQ ID NO: 279), CTL2gam-21 (SEQ ID NO: 278), CTL2gam-23 (SEQ ID NO: 277), CTL2gam-24 (SEQ ID NO: 276), CTL2gam-26 (SEQ ID NO: 275), CTL2gam-27 (SEQ ID NO: 274), CTL2gam-28 (SEQ ID NO: 273), CTL2gam-30-3' (SEQ ID NO: 272, a second determined genomic sequence

representing the 3' end) and CTL2gam-30-5' (SEQ ID NO: 271, a first determined genomic sequence representing the 5' end).

EXAMPLE 2

INDUCTION OF T CELL PROLIFERATION AND INTERFERON-γ PRODUCTION BY *CHLAMYDIA TRACHOMATIS* ANTIGENS

The ability of recombinant *Chlamydia trachomatis* antigens to induce T cell proliferation and interferon-γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatograph (Webb et al., *J. Immunology 157*:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. trachomatis* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μg/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 μg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μl, 50 μl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN-γ is measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN-γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN-γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The

plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

Using the above methodology, recombinant 1B1-66 protein (SEQ ID NO: 5) as well as two synthetic peptides corresponding to amino acid residues 48-67 (SEQ ID NO: 13; referred to as 1-B1-66/48-67) and 58-77 (SEQ ID NO: 14, referred to as 1B1-66/58-77), respectively, of SEQ ID NO: 5, were found to induce a proliferative response and IFN-γ production in a Chlamydia-specific T cell line used to screen a genomic library of *C. trachomatis* LGV II.

Further studies have identified a *C. trachomatis*-specific T-cell epitope in the ribosomal S13 protein. Employing standard epitope mapping techniques well known in the art, two T-cell epitopes in the ribosomal S13 protein (rS13) were identified with a *Chlamydia*-specific T-cell line from donor CL-8 (T-cell line TCL-8 EB/DC). Fig. 8 illustrates that the first peptide, rS13 1-20 (SEQ ID NO: 106), is 100% identical with the corresponding *C. pneumoniae* sequence, explaining the cross-reactivity of the T-cell line to recombinant *C. trachomatis*- and *C. pneumoniae*-rS13. The response to the second peptide rS13 56-75 (SEQ ID NO: 108) is *C. trachomatis*-specific, indicating that the rS13 response in this healthy asymptomatic donor was elicited by exposure to *C. trachomatis* and not to *C. pneumoniae*, or any other microbial infection.

As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5 x 10^4 TCP-21 T-cells in the presence of 1 x 10^4 monocyte-derived dendritic cells

with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae.*

To further define the epitope described above, an additional T-cell line, TCT-3, was used in epitope mapping experiments. The immunoassays were performed as described above, except that only peptides from *C. trachomatis* were tested. The T-cells gave a proliferative response to two peptides, CT-OMCB #152-171 and CT-OMCB #157-176 (SEQ ID NO: 246 and 247, respectively), thereby defining an additional immunogenic epitope in the cysteine rich outer membrane protein of *C. trachomatis.*

Clone 14H1-4, (SEQ ID NO: 56, with the corresponding full-length amino acid sequence provided in SEQ ID NO: 92), was identified using the TCT-3 cell line in the CD4 T-cell expression cloning system previously described, and was shown to contain a complete ORF for the, thiol specific antioxidant gene (CT603), referred to as TSA. Epitope mapping immunoassays were performed, as described above, to further define the epitope. The TCT-3 T-cells line exhibited a strong proliferative response to the overlapping peptides CT-TSA #96-115, CT-TSA #101-120 and CT-TSA #106-125 (SEQ ID NO: 254-256, respectively) demonstrating an immunoreactive epitope in the thiol specific antioxidant gene of *C. trachomatis* serovar LGVII.

EXAMPLE 3

PREPARATION OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugating or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 4

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING *CHLAMYDIA* ANTIGENS USING RETROVIRAL EXPRESSION VECTOR SYSTEMS AND SUBSEQUENT IMMUNOLOGICAL ANALYSIS

A genomic library of *Chlamydia trachomatis* LGV II was constructed by limited digests using BamHI, BglII, BstYi and MboI restriction enzymes. The restriction digest fragments were subsequently ligated into the BamHI site of the retroviral vectors pBIB-KS1,2,3. This vector set was modified to contain a Kosak translation initiation site and stop codons in order to allow expression of proteins from short DNA genomic fragments, as shown in Fig. 2. DNA pools of 80 clones were prepared and transfected into the retroviral packaging line Phoenix-Ampho, as described in Pear, W.S., Scott, M.L. and Nolan, G.P., Generation of High Titre, Helper-free Retroviruses by Transient Transfection. Methods in Molecular Medicine: Gene

Therapy Protocols, Humana Press, Totowa, NJ, pp. 41-57. The *Chlamydia* library in retroviral form was then transduced into H2-Ld expressing P815 cells, which were then used as target cells to stimulate an antigen specific T-cell line.

A *Chlamydia*-specific, murine $H2^d$ restricted CD8+ T-cell line was expanded in culture by repeated rounds of stimulation with irradiated *C. trachomatis*-infected J774 cells and irradiated syngeneic spleen cells, as described by Starnbach, M., in *J. Immunol.*, 153:5183, 1994. This *Chlamydia*-specific T-cell line was used to screen the above *Chlamydia* genomic library expressed by the retrovirally-transduced P815 cells. Positive DNA pools were identified by detection of IFN-γ production using Elispot analysis (*SEE* Lalvani et al., *J. Experimental Medicine 186*:859-865, 1997).

Two positive pools, referred to as 2C7 and 2E10, were identified by IFN-γ Elispot assays. Stable transductants of P815 cells from pool 2C7 were cloned by limiting dilution and individual clones were selected based upon their capacity to elicit IFN-γ production from the *Chlamydia*-specific CTL line. From this screening process, four positive clones were selected, referred to as 2C7-8, 2C7-9, 2C7-19 and 2C7-21. Similarly, the positive pool 2E10 was further screened, resulting in an additional positive clone, which contains three inserts. The three inserts are fragments of the CT016, tRNA syntase and clpX genes (SEQ ID NO: 268-270, respectively).

Transgenic DNA from these four positive 2C7 clones were PCR amplified using pBIB-KS specific primers to selectively amplify the *Chlamydia* DNA insert. Amplified inserts were gel purified and sequenced. One immunoreactive clone, 2C7-8 (SEQ ID NO: 15, with the predicted amino acid sequence provided in SEQ ID NO: 32), is a 160 bp fragment with homology to nucleotides 597304-597145 of *Chlamydia trachomatis*, serovar D (NCBI, BLASTN search; SEQ ID NO: 33, with the predicted amino acid sequence provided in SEQ ID NO: 34). The sequence of clone 2C7-8 maps within two putative open reading frames from the region of high homology described immediately above, and in particular, one of these putative open reading frames, consisting of a 298 amino acid fragment (SEQ ID NO: 16, with the predicted amino acid sequence provided in SEQ ID NO: 17), was demonstrated to exhibit immunological activity.

Full-length cloning of the 298 amino acid fragment (referred to as CT529 and/or the Cap1 gene) from serovar L2 was obtained by PCR amplification using 5'-

ttttgaageaggtaggtgaatatg (forward) (SEQ ID NO: 159) and 5'-ttaagaaatttaaaaaatccctta (reverse) (SEQ ID NO: 160) primers, using purified *C. trachomatis* L2 genomic DNA as template. This PCR product was gel-purified, cloned into pCRBlunt (Invitrogen, Carlsbad, CA) for sequencing, and then subcloned into the *Eco*RI site of pBIB-KMS, a derivative of pBIB-KS for expression. The *Chlamydia pnuemoniae* homlogue of CT529 is provided in SEQ ID NO: 291, with the corresponding amino acid sequence provided in SEQ ID NO: 292.

Full-length DNA encoding various CT529 serovars were amplified by PCR from bacterial lysates containing 10^5 IFU, essentially as described (Denamur, E., C. Sayada, A. Souriau, J. Orfila, A. Rodolakis and J. Elion. 1991. J. Gen. Microbiol. 137: 2525). The following serovars were amplified as described: Ba (SEQ ID NO: 134, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 135); E (BOUR) and E (MTW447) (SEQ ID NO: 122, with the corresponding predieted amino acid sequence provided in SEQ ID NO: 123); F (NI1) (SEQ ID NO: 128, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 129); G; (SEQ ID NO: 126, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 127); Ia (SEQ ID NO: 124, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 125); L1 (SEQ ID NO: 130, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 131); L3 (SEQ ID NO: 132, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 133); I (SEQ ID NO: 263, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 264); K (SEQ ID NO: 265, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 266); and MoPn (SEQ ID NO: 136, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 137). PCR reactions were performed with Advantage Genomic PCR Kit (Clontech, Palo Alto, CA) using primers specific for serovar L2 DNA (external to the ORF). Primers sequences were 5'-ggtataatatctctctaaattttg (forward-SEQ ID NO: 161) and 5'-agataaaaaaggctgtttc' (reverse-SEQ ID NO: 162) except for MoPn which required 5'-ttttgaagcaggtaggtgaatatg (forward-SEQ ID NO: 163) and 5'-tttacaataagaaaagctaagcactttgt (reverse-SEQ ID NO: 164). PCR amplified DNA was purified with QIAquick PCR purifieation kit (Qiagen, Valencia, CA) and cloned in pCR2.1 (Invitrogen, Carlsbad, CA) for sequencing.

Sequencing of DNA derived from PCR amplified inserts of immunoreactive clones was done on an automated sequencer (ABI 377) using both a pBIB-KS specific forward primer 5'-ccttacacagtcctgctgac (SEQ ID NO: 165) and a reverse primer 3'-gtttccgggccctcacattg (SEQ ID NO: 166). PCRBlunt cloned DNA coding for CT529 serovar L2 and pCR2.1 cloned DNA coding for CT529 serovar Ba, E (BOUR), E (MTW447), F (NI1), G, Ia, K, L1, L3 and MoPn were sequenced using T7 promoter primer and universal M13 forward and M13 reverse primers.

To determine if these two putative open reading frames (SEQ ID NO: 16 and 20) encoded a protein with an associated immunological function, overlapping peptides (17-20 amino acid lengths) spanning the lengths of the two open reading frames were synthesized, as described in Example 3. A standard chromium release assay was utilized to determine the percent specific lysis of peptide-pulsed $H2^d$ restricted target cells. In this assay, aliquots of P815 cells ($H2^d$) were labeled at 37° C for one hour with 100 μCi of ^{51}Cr in the presence or absence of 1 μg/ml of the indicated peptides. Following this incubation, labeled P815 cells were washed to remove excess ^{51}Cr and peptide, and subsequently plated in duplicate in microculture plates at a concentration of 1,000 cells/well. Effector CTL (*Chlamydia*-specific CD8 T cells) were added at the indicated effeetor:target ratios. Following a 4 hour incubation, supernatants were harvested and measured by gamma-counter for release of ^{51}Cr into the supernatant. Two overlapping peptides from the 298 amino acid open reading frame did specifically stimulate the CTL line. The peptides represented in SEQ ID NO: 138-156 were synthesized, representing the translation of the L2 homologue of the serovar D open reading frame for CT529 (Cap1 gene) and 216 amino acid open reading frame. As shown in Fig. 3, peptides CtC7.8-12 (SEQ ID NO: 18, also referred to as Cap1#132-147, SEQ ID NO: 139) and CtC7.8-13 (SEQ ID NO: 19, also referred to as Cap1#138-155, SEQ ID NO: 140) were able to elicit 38 to 52% specific lysis, respectively, at an effector to target ratio of 10:1. Notably, the overlap between these two peptides contained a predicted $H2^d$ (K^d and L^d) binding peptide. A 10 amino acid peptide was synthesized to correspond to this overlapping sequence (SEQ ID NO: 31) and was found to generate a strong immune response from the anti-*Chlamydia* CTL line by elispot assay. Significantly, a search of the most recent Genbank database revealed no proteins have previously been described for this gene. Therefore, the putative open

reading frame encoding clone 2C7-8 (SEQ ID NO: 15) defines a gene which encompasses an antigen from *Chlamydia* capable of stimulating antigen-specific CD8+ T-cells in a MHC-I restricted manner, demonstrating this antigen could be used to develop a vaccine against *Chlamydia*.

To confirm these results and to further map the epitope, truncated peptides (SEQ ID NO: 138-156) were made and tested for recognition by the T-cells in an IFN-g ELISPOT assay. Truncations of either Ser139 (Cap1#140-147, SEQ ID NO: 146) or Leu147 (Cap1#138-146, SEQ ID NO: 147) abrogate T-cell recognition. These results indicate that the 9-mer peptide Cap1#139-147 (SFIGGITYL, SEQ ID NO: 145) is the minimal epitope recognized by the *Chlamydia*-specific T-cells.

Sequence alignments of Capl (CT529) from selected serovars of *C. trachomatis* (SEQ ID NO: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139) shows one of the amino acid differences is found in position 2 of the proposed epitope. The homologous serovar D peptide is SIIGGITYL (SEQ ID NO: 168). The ability of SFIGGITYL and SIIGGITYL to target cells for recognition by the *Chlamydia* specific T-cells was compared. Serial dilutions of each peptide were incubated with P815 cells and tested for recognition by the T-cells in a ^{51}Cr release assay, as described above. The *Chlamydia*-specific T-cells recognize the serovar L2 peptide at a minimum concentration of 1 nM and the serovar D peptide at a minimum concentration of 10 nM.

Further studies have shown that a Cap1#139-147-specific T-cell clone recognizes *C. trachomatis* infected cells. To confirm that $Cap1_{139\text{-}147}$ is presented on the surface of *Chlamydia* infected cells, Balb-3T3 (H-2^{d}) cells were infected with *C. trachomatis* serovar L2 and tested to determine whether these cells are recognized by a CD8+ T-cell clone specific for Cap1#139-147 epitope (SEQ ID NO: 145). The T-cell clone specific for Cap1#139-147 epitope was obtained by limiting dilution of the line 69 T-cells. The T-cell clone specifically recognized the *Chlamydia* infected cells. In these experiments, target cells were *C. trachomatis* infected (positive control) or uninfected Balb/3T3 cells, showing 45%, 36% and 30% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively; or Cap1#139-147 epitope (SEQ ID NO: 145) coated, or untreated P815 cells, showing 83%, 75% and 58% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively (negative controls having less than 5% lysis in all cases). This data suggests that the epitope is presented during infection.

In vivo studies show Cap1#139-147 epitope-specific T-cells are primed during murine infection with *C. trachomatis*. To determine if infection with *C. trachomatis* primes a Cap1#139-147 epitope-specific T-cell response, mice were infected i.p. with 10^8 IFU of *C. trachomatis* serovar L2. Two weeks after infection, the mice were sacrificed and spleen cells were stimulated on irradiated syngeneic spleen cells pulsed with Cap1#139-147 epitope peptide. After 5 days of stimulation, the cultures were used in a standard ^{51}Cr release assay to determine if there were Cap1#139-147 epitope-specific T-cells present in the culture. Specifically, spleen cells from a *C. trachomatis* serovar L2 immunized mouse or a control mouse injected with PBS after a 5 days culture with Cap1#139-147 peptide-coated syngeneic spleen cells and CD8+ T-cells able to specifically recognize Cap1#139-147 epitope gave 73%, 60% and 32% specific lysis at a30:1, 10:1 and 3:1 effector to target ratios, respectively. The control mice had a percent lysis of approximately 10% at a 30:1 effector to target ratio, and steadily declining with lowering E:T ratios. Target cells were Cap1#139-147 peptide-coated, or untreated P815 cells. These data suggest that Cap1#139-147 peptide-specific T-cells are primed during murine infection with *C. trachomatis*.

Ct529 Localization

Studies were performed demonstrating that Ct529 (referred to herein as Cap-1) localizes to the inclusion membrane of *C. trachomatis*-infected cells and is not associated with elementary bodies or reticulate bodies. As described above, Cap-1 was identified as a product from *Chlamydia* that stimulates CD8+ CTL. These CTL are protective in a murine model of infection, thus making Cap-1 a good vaccine candidate. Further, since these CTL are MHC-I restricted, the Cap-1 gene must have access to the cytosol of infected cells, which may be a unique characteristic of specific *Chlamydial* gene products. Therefore, determination of the cellular localization of the gene products would be useful in characterizing Cap-1 as a vaccine candidate. To detect the intracellular localization of Cap-1, rabbit polyclonal antibodies directed against a recombinant polypeptide encompassing the N-terminal 125 amino acids of Cap-1 (SEQ ID NO: 305, with the amino acid sequence including the N-terminal 6-His tag provided in SEQ ID NO: 304) were used to stain McCoy cells infected with *Chlamydiae*.

Rabbit-anti-Cap-1 polyclonal antibodies were obtained by hyper-immunization of rabbits with a recombinant polypeptide, rCt529c1-125 (SEQ ID NO: 305) encompassing the N-terminal portion of Cap-1. Recombinant rCt529e1-125 protein was obtained from *E. coli* transformed with a pET expression plasmid (as described above) encoding the nucleotides 1-375 encoding the N-terminal 1-125 amino acids of Cap-1. Recombinant protein was purified by Ni-NTA using techniques well known in the art. For a positive control antiserum, polyclonal antisera directed against elementary bodies were made by immunization of rabbits with purified *C. trachomatis* elementary bodies (Biodesign, Sacco, Maine). Pre-immune sera derived from rabbits prior to immunization with the Cap-1 polypeptide was used as a negative control.

Immunocytochemistry was performed on McCoy cell monolayers grown on glass coverslips inoculated with either *C. trachomatis* serovar L2 or *C. psitacci*, strain 6BC, at a concentration of 10^6 IFU (Inclusion Forming Units) per ml. After 2 hours, medium was aspirated and replaced with fresh RP-10 medium supplemented with cycloheximide (1.0 μg/ml). Infected cells were incubated at in 7% CO_2 for 24 hours and fixed by aspirating medium, rinsing cells once with PBS and methanol fixation for 5 minutes. For antigen staining, fixed cell monolayers were washed with PBS and incubated at 37°C for 2 hours with 1:100 dilutions of specific or control antisera. Cells were rinsed with PBS and incubated for 1 hour with fluorescein isothiocyanate (FITC)-labeled, anti-rabbit IgG (KPL, Gaithersburg) and stained with Evans blue (0.05%) in PBS. Fluorescence was observed with a 100X objective (Zeiss epifluorescence microscope), and photographed (Nikon UFX-11A camera).

Results from this study show Cap-1 localizes to the inclusion membrane of *C. trachomatis*-infected cells. Cap-1 specific antibody labeled the inclusion membranes of *C. trachomatis*-infected cells, but not *Chlamydial* elementary bodies contained in these inclusions or released by the fixation process. Conversely, the anti-elementary body antibody clearly labeled the bacterial bodies, not only within the inclusions, but those released by the fixation process. Specificity of the anti-Cap-1 antibody is demonstrated by the fact that it does not stain *C. psittaci*-infected cells. Specificity of the Cap-1 labeling is also shown by the absence of reactivity in pre-immune sera. These results suggest that Cap-1 is released from the bacteria and becomes associated with the *Chlamydial* inclusion membrane. Therefore, Cap-1 is a

gene product which may be useful for stimulating CD8+ T cells in the development of a vaccine against infections caused by *Chlamydia*.

The relevance of the Cap-1 gene as a potential CTL antigen in a vaccine against *Chlamydia* infection is further illustrated by two additional series of studies. First, CTL specific for the MHC-I epitope of Cap-1 CT529 #138-147 peptide of *C. trachomatis* (SEQ ID NO: 144) have been shown to be primed to a high frequency during natural infection. Specifically, Balb/C mice were inoculated with 10^6 I.F.U. of *C. trachomatis*, serova L2. After 2 weeks, spleens were harvested and quantified by Elispot analysis for the number of IFN-γ secreting cells in response to Cap-1 #138-147 peptide-pulsed antigen presenting cells. In two experiments, the number of IFN-γ-secreting cells in 10^5 splenocytes was about 1% of all CD8+ T-cells. This high frequency of responding CD8+ CTL to the MHC-1 epitope (Cap-1 CT529 #138-147 peptide) suggest that Cap-1 is highly immunogenic in infections.

Results from a second series of studies have shown that the Cap-1 protein is almost immediately accessible to the cytosol of the host cell upon infection. This is shown in a time-course of Cap-1 CT529 #138-147 peptide presentation. Briefly, 3T3 cells were infected with *C. trachomatis* serovar L2 for various lengths of time, and then tested for recognition by Cap-1 CT529 #138-147 peptide-specific CTL. The results show that *C. trachomatis*-infected 3T3 cells are targeted for recognition by the antigen-specific CTL after only 2 hours of infection. These results suggest that Cap-1 is an early protein synthesized in the development of *C. trachomatis* elementary bodies to reticulate bodies. A CD8+ CTL immune response directed against a gene product expressed early in infection may be particularly efficacious in a vaccine against *Chlamydia* infection.

EXAMPLE 5

GENERATION OF ANTIBODY AND T-CELL RESPONSES IN MICE IMMUNIZED WITH *CHLAMYDIA* ANTIGENS

Immunogenicity studies were conducted to determine the antibody and CD4+ T cell responses in mice immunized with either purified SWIB or S13 proteins formulated with Montanide adjuvant, or DNA-based immunizations with pcDNA-3 expression

vectors containing the DNA sequences for SWIB or S13. SWIB is also referred to as clone 1-B1-66 (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5), and S13 ribosomal protein is also referred to as clone 10-C10-31 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12). In the first experiment, groups of three C57BL/6 mice were immunized twice and monitored for antibody and CD4+ T-cell responses. DNA immunizations were intradermal at the base of the tail and polypeptide immunizations were administered by subcutaneous route. Results from standard ^{3}H-incorporation assays of spleen cells from immunized mice shows a strong proliferative response from the group immunized with purified recombinant SWIB polypeptide (SEQ ID NO: 5). Further analysis by cytokine induction assays, as previously described, demonstrated that the group immunized with SWIB polypeptide produced a measurable IFN-γ and IL-4 response. Subsequent ELISA-based assays to determine the predominant antibody isotype response in the experimental group immunized with the SWIB polypeptide were performed. Fig. 4 illustrates the SWIB-immunized group gave a humoral response that was predominantly IgG1.

In a second experiment, C3H mice were immunized three times with 10 μg purified SWIB protein (also referred to as clone 1-B1-66, SEQ ID NO: 5) formulated in either PBS or Montanide at three week intervals and harvested two weeks after the third immunization. Antibody titers directed against the SWIB protein were determined by standard ELISA-based techniques well known in the art, demonstrating the SWIB protein formulated with Montanide adjuvant induced a strong humoral immune response. T-cell proliferative responses were determined by a XTT-based assay (Scudiero, et al, *Cancer Research*, 1988, 48:4827). As shown in Fig. 5, splenocytes from mice immunized with the SWIB polypeptide plus Montanide elicited an antigen specific proliferative response. In addition, the capacity of splenocytes from immunized animals to secrete IFN-γ in response to soluble recombinant SWIB polypeptide was determined using the cytokine induction assay previously described. The splenocytes from all animals in the group immunized with SWIB polypeptide formulated with montanide adjuvant secreted IFN-γ in response to exposure to the SWIB Chlamydia antigen, demonstrating an *Chlamydia*-specific immune response.

In a further experiment, C3H mice were immunized at three separate time points at the base of the tail with 10 μg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) formulated with the SBAS2 adjuvant (SmithKline Beecham, London, England). Antigen-specific antibody titers were measured by ELISA, showing both polypeptides induced a strong IgG response, ranging in titers from 1 $x10^{-4}$ to 1 $x10^{-5}$. The IgG1 and IgG2a components of this response were present in fairly equal amounts. Antigen-specific T-cell proliferative responses, determined by standard ^{3}H-incorporation assays on spleen cells isolated from immunized mice, were quite strong for SWIB (50,000 cpm above the negative control) and even stronger for s13 (100,000 cpm above the negative control). The IFNγ production was assayed by standard ELISA techniques from supernatant from the proliferating culture. *In vitro* restimulation of the culture with S13 protein induced high levels of IFNγ production, approximately 25 ng/ml versus 2 ng/ml for the negative control. Restimulation with the SWIB protein also induced IFNγ, although to a lesser extent.

In a related experiment, C3H mice were immunized at three separate time points with 10 μg of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) mixed with 10 μg of Cholera Toxin. Mucosal immunization was through intranasal inoculation. Antigen-specific antibody responses were determined by standard ELISA techniques. Antigen-specific IgG antibodies were present in the blood of SWIB-immunized mice, with titers ranging from 1 $x10^{-3}$ to 1 $x10^{-4}$, but non-detectable in the S13-immunized animals. Antigen-specific T-cell responses from isolated splenocytes, as measured by IFNγ production, gave similar results to those described immediately above for systemic immunization.

An animal study was conducted to determine the immunogenicity of the CT529 serovar LGVII CTL epitope, defined by the CT529 10mer consensus peptide (CSFIGGITYL – SEQ ID NO: 31), which was identified as an H2-Kd restricted CTL epitope. BALB/c mice (3 mice per group) were immunized three times with 25 μg of peptide combined with various adjuvants. The peptide was administered systemically at the base of the tail in either SKB Adjuvant System SBAS-2", SBAS-7 (SmithKline

Beecham, London, England) or Montanide. The peptide was also administered intranasally mixed with 10ug of Cholera Toxin (CT). Naive mice were used as a control. Four weeks after the 3rd immunization, spleen cells were restimulated with LPS-blasts pulsed with 10ug/ml CT529 10mer consensus peptide at three different effector to LPS-blasts ratios : 6, 1.5 and 0.4 at $1x10^6$ cell/ml. After 2 restimulations, effector cells were tested for their ability to lyse peptide pulsed P815 cells using a standard chromium release assay. A non-relevant peptide from chicken egg ovalbumin was used as a negative control. The results demonstrate that a significant immune response was elicited towards the CT529 10mer consensus peptide and that antigen-specific T-cells capable of lysing peptide-pulsed targets were elicited in response to immunization with the peptide. Specifically, antigen-specific lytic activities were found in the SBAS-7 and CT adjuvanted group while Montanide and SBAS-2" failed to adjuvant the CTL epitope immunization.

EXAMPLE 6

EXPRESSION AND CHARACTERIZATION OF *CHLAMYDIA PNEUMONIAE* GENES

The human T-cell line, TCL-8, described in Example 1, recognizes *Chlamydia trachomatis* as well as *Chlamydia pneumonia* infected monocyte-derived dendritic cells, suggesting *Chlamydia trachomatis* and *pneumonia* may encode cross-reactive T-cell epitopes. To isolate the *Chlamydia pneumonia* genes homologous to *Chlamydia trachomatis* LGV II clones 1B1-66, also referred to as SWIB (SEQ ID NO: 1) and clone 10C10-31, also referred to as S13 ribosomal protein (SEQ ID NO: 4), HeLa 229 cells were infected with *C. pneumonia* strain TWAR (CDC/CWL-029). After three days incubation, the *C. pneumonia*-infected HeLa cells were harvested, washed and resuspended in 200 μl water and heated in a boiling water bath for 20 minutes. Ten microliters of the disrupted cell suspension was used as the PCR template.

C. pneumonia specific primers were designed for clones 1B1-66 and 10C10-31 such that the 5' end had a 6X-Histidine tag and a Nde I site inserted, and the 3' end had a stop codon and a BamHI site included (Fig. 6). The PCR products were amplified and sequenced by standard techniques well known in the art. The *C.*

pneumonia-specific PCR products were cloned into expression vector pET17B (Novagen, Madison, WI) and transfected into E. coli BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Two proteins from *C. pneumonia* were thus generated, a 10-11 kDa protein referred to as CpSWIB (SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively), a 15 kDa protein referred to as CpS13 (SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively).

EXAMPLE 7

INDUCTION OF T CELL PROLIFERATION AND INTERFERON-γ PRODUCTION BY *CHLAMYDIA PNEUMONIAE* ANTIGENS

The ability of recombinant *Chlamydia pneumoniae* antigens to induce T cell proliferation and interferon-γ production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatography (Webb et al., *J. Immunology 157*:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. pneumoniae* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 µg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 µl, 50 µl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 µCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN-γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN-γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN-γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

A human anti-*Chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* was used to determine whether the expressed proteins described in the example above, (i.e., CpSWIB, SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively, and the 15 kDa protein referred to as CpS13 SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively), possessed T-cell epitopes common to both *C. trachomatis* and *C. pneumonia.* Briefly, *E. coli* expressing *Chlamydial* proteins were titered on 1 x 10^4 monocyte-derived dendritic cells. After two hours, the dendritic_cells cultures were washed and 2.5 x 10^4 T cells (TCL-8) added and allowed to incubate for an additional 72 hours. The amount of INF-γ in the culture supernatant was then determined by ELISA. As shown in Figs. 7A and 7B, the TCL-8 T-cell line specifically recognized the S13 ribosomal protein from both *C. trachomatis* and *C. pneumonia* as demonstrated by the antigen-specific induction of IFN-γ, whereas only the SWIB protein from *C. trachomatis* was recognized by the T-cell line. To

validate these results, the T cell epitope of *C. trachomatis* SWIB was identified by epitope mapping using target cells pulsed with a series of overlapping peptides and the T-cell line TCL-8. 3H-thymidine incorporation assays demonstrated that the peptide, referred to as C.t.SWIB 52-67, of SEQ ID NO: 39 gave the strongest proliferation of the TCL-8 line. The homologous peptides corresponding to the SWIB of *C. pneumoniae* sequence (SEQ ID NO: 40), the topoisomerase-SWIB fusion of *C. pneumoniae* (SEQ ID NO: 43) and *C. trachomatis* (SEQ ID NO: 42) as well as the human SWI domain (SEQ ID NO: 41) were synthesized and tested in the above assay. The T-cell line TCL-8 only recognized the *C. trachomatis* peptide of SEQ ID NO: 39 and not the corresponding *C. pneumoniae* peptide (SEQ ID NO: 40), or the other corresponding peptides described above (SEQ ID NO; 41-43).

Chlamydia-specific T cell lines were generated from donor CP-21 with a positive serum titer against *C. pneumoniae* by stimulating donor PBMC with either *C. trachomatis* or *C. pneumoniae*-infected monocyte-derived dendritic cells, respectively. T-cells generated against *C. pneumoniae* responded to recombinant *C. pneumoniae*-SWIB but not *C. trachomatis*-SWIB, whereas the T-cell line generated against *C. trachomatis* did not respond to either *C. trachomatis*- or *C. pneumoniae*-SWIB (see Fig. 9). The *C. pneumoniae*-SWIB specific immune response of donor CP-21 confirms the *C. pneumoniae* infection and indicates the elicitation of *C. pneumoniae*-SWIB specific T-cells during *in vivo C. pneumoniae* infection.

Epitope mapping of the T-cell response to *C. pneumoniae*-SWIB has shown that Cp-SWIB-specific T-cells responded to the overlapping peptides Cp-SWIB 32-51 (SEQ ID NO: 101) and Cp-SWIB 37-56 (SEQ ID NO: 102), indicating a *C. pneumoniae*-SWIB-specific T-cell epitope Cp-SWIB 37-51 (SEQ ID NO: 100).

In additional experiments, T-cell lines were generated from donor CP1, also a *C. pneumoniae* seropositive donor, by stimulating PBMC with non-infectious elementary bodies from *C. trachomatis* and *C. pneumoniae*, respectively. In particular, proliferative responses were determined by stimulating 2.5 x 10^4 T-cells in the presence of 1 x 10^4 monocyte-derived dendritic cells and non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or either recombinant *C. trachomatis* or *C. pneumoniae* SWIB protein. The T-cell response against SWIB resembled the data obtained with T-cell lines from CP-21 in that *C. pneumoniae*-SWIB, but not *C.*

trachomatis-SWIB elicited a response by the *C. pneumoniae* T-cell line. In addition, the *C. trachomatis* T-cell line did not proliferate in response to either *C. trachomatis* or *C. pneumoniae* SWIB, though it did proliferate in response to both CT and CP elementary bodies.As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 eell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMCB. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating 2.5 x 10^4 TCP-21 T-cells in the presence of 1 x 10^4 monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae,* or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMCB protein (0.1 μg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-eell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae.*

EXAMPLE 8

IMMUNE RESPONSES OF HUMAN PBMC AND T-CELL LINES AGAINST *CHLAMYDIA* ANTIGENS

The examples provided herein suggest that there is a population of healthy donors among the general population that have been infected with *C. trachomatis* and generated a protective immune response controlling the *C. trachomatis* infection. These donors remained clinically asymptomatic and seronegative for *C. trachomatis*. To characterize the immune responses of normal donors against *chlamydial* antigens which had been identified by CD4 expression cloning, PBMC

obtained from 12 healthy donors were tested against a panel of recombinant *chlamydial* antigens including *C. trachomatis-, C. pneumoniae*-SWIB and *C. trachomatis-, C. pneumoniae*-S13. The data are summarized in Table I below. All donors were seronegative for *C. trachomatis*, whereas 6/12 had a positive *C. pneumoniae* titer. Using a stimulation index of >4 as a positive response, 11/12 of the subjects responded to *C. trachomatis* elementary bodies and 12/12 responded to *C. pneumoniae* elementary bodies. One donor, AD104, responded to recombinant *C. pneumoniae*-S13 protein, but not to recombinant *C. trachomatis*-S13 protein, indicating a *C. pneumoniae*-specific response. Three out of 12 donors had a *C. trachomatis*-SWIB, but not a *C. pneumoniae*-SWIB specific response, confirming a *C. trachomatis* infection. *C. trachomatis* and *C. pneumoniae*- S13 elicited a response in 8/12 donors suggesting a chlamydial infection. These data demonstrate the ability of SWIB and S13 to elicit a T-cell response in PBMC of normal study subjects.

Table I.

Immune response of normal study subjects against *Chlamydia*

Donor	Sex	*Chlamydia* IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
AD100	male	negative	++	+++	+	-	++	++	-	n.t.
AD104	female	negative	+++	++	-	-	-	++	-	n.t.
AD108	male	CP 1:256	++	++	+	+/-	+	+	+	n.t.
AD112	female	negative	++	++	+	-	+	-	+/-	n.t.
AD120	male	negative	-	+	-	-	-	-	-	n.t.
AD124	female	CP 1:128	++	++	-	-	-	-	-	n.t.
AD128	male	CP 1:512	+	++	-	-	++	+	++	-
AD132	female	negative	++	++	-	-	+	+	-	-
AD136	female	CP 1:128	+	++	-	-	+/-	-	-	-
AD140	male	CP 1:256	++	++	-	-	+	+	-	-
AD142	female	CP 1:512	++	++	-	-	+	+	+	-
AD146	female	negative	++	++	-	-	++	+	+	-

CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae;* EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein.Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3 x 10^5 PBMC with 1 x 10^4 monocyte-derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^{3}H-thymidine pulse for the last 18h.

SI: Stimulation index

+/-:	SI ~	4
+:	SI >	4
++:	SI	10-30
+++:	SI >	30

In a first series of experiments, T-cell lines were generated from a healthy female individual (CT-10) with a history of genital exposure to *C. trachomatis* by stimulating T-cells with *C. trachomatis* LGV II elementary bodies as previously described. Although the study subject was exposed to *C. trachomatis*, she did not seroconvert and did not develop clinical symptoms, suggesting donor CT-10 may have developed a protective immune response against *C. trachomatis*. As shown in Fig. 10, a primary *Chlamydia*-specific T-cell line derived from donor CT-10 responded to *C. trachomatis*-SWIB, but not *C. pneumoniae*-SWIB recombinant proteins, confirming the exposure of CT-10 to *C. trachomatis*. Epitope mapping of the T-cell response to *C. trachomatis*-SWIB showed that this donor responded to the same epitope Ct-SWIB 52-67 (SEQ ID NO: 39) as T-cell line TCL-8, as shown in Fig. 11.

Additional T-cell lines were generated as described above for various *C. trachomatis* patients. A summary of the patients' clinical profile and proliferative responses to various *C. trachomatis* and *C. pneumoniae* elementary bodies and recombinant proteins are summarized in Table II as follows:

Proliferative response of *C. trachomatis* patients

Patients	Clinical manifestation	IgG titer	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
CT-1	NGU	negative	+	+	-	-	++	++	++	+
CT-2	NGU	negative	++	++	-	-	+	+/-	-	-
CT-3	asymptomatic shed Eb Dx was HPV	Ct 1:512 Cp 1:1024 Cps 1:256	+	+	-	-	+	-	+	-
CT-4	asymptomatic shed Eb	Ct 1:1024	+	+	-	-	-	-	-	-
CT-5	BV	Ct 1:256 Cp 1:256	++	++	-	-	+	-	-	-
CT-6	perinial rash discharge	Cp 1:1024	+	+	-	-	-	-	-	-
CT-7	BV genital ulcer	Ct 1:512 Cp 1:1024	+	+	-	-	+	+	+	-
CT-8	Not known	Not tested	++	++	-	-	-	-	-	-
CT-9	asymptomatic	Ct 1:128 Cp 1:128	+++	++	-	-	++	+	+	-
CT-10	Itch mild vulvar	negative	++	++	-	-	-	-	-	-
CT-11	BV, abnormal pap	Ct 1: 512	+++	+++	-	-	+++	+/-	++	+
CT-12	asymptomatic	Cp 1: 512	++	++	-	-	++	+	+	-

NGU= Non-Gonococcal Urethritis; BV= Bacterial Vaginosis; CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae;* EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein

Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating 3 x 10^5 PBMC with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a ^{3}H-thymidine pulse for the last 18 hours.

SI: Stimulation index

+/-: SI ~ 4
+: SI > 4
++: SI 10-30
+++: SI > 30

Using the panel of asymptomatic (as defined above) study subjects and *C. trachomatis* patients, as summarized in Tables I and II, a comprehensive study of the immune responses of PBMC derived from the two groups was conducted. Briefly, PBMCs from *C. pneumoniae* patients as well as from normal donors are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 μ g/ml gentamicin. Purified polypeptides, a panel of recombinant *chlamydial* antigens including *C. trachomatis-, C. pneumoniae*-SWIB and S13, as well as . *C. trachomatis* lpdA and TSA are added in duplicate at concentrations of 0.5 to 10 μg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 μl, 50 μl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 μCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

Proliferative responses to the recombinant *Chlamydiae* antigens demonstrated that the majority of asymptomatic donors and *C. trachomatis* patients recognized the *C. trachomatis* S13 antigen (8/12) and a majority of the *C. trachomatis* patients recognized the *C. pneumonia* S13 antigen (8/12), with 4/12 asymptomatic donors also recognizing the *C. pneumonia* S13 antigen. Also, six out of twelve of the *C. trachomatis* patients and four out of twelve of the asymptomatic donors gave a proliferative response to the lpdA antigen of *C. trachomatis*. These results demonstrate that the *C. trachomatis* and *C. pneumonia* S13 antigen, *C. trachomatis* Swib antigen and the *C. trachomatis* lpdA antigen are recognized by the asymptomatic donors, indicating these antigens were recognized during exposure to *Chlamydia* and an immune response elicited against them. This implies these antigens may play a role in conferring protective immunity in a human host. In addition, the *C. trachomatis* and *C. pneumonia* S13 antigen is recognized equally well among the *C. trachomatis* patients, therefore indicating there may be epitopes shared between *C. trachomatis* and *C. pneumonia* in the S13 protein. Table III summarizes the results of these studies.

Table III.

Antigen	Normal Donors	C.t. Patients
C.t.-Swib	3/12	0/12
C.p.-Swib	0/12	0/12
C.t.-S13	8/12	8/12
C.p.-S13	4/12	8/12
lpdA	4/12	6/12
TSA	0/12	2/12

A series of studies were initiated to determine the cellular immune response to short-term T-cell lines generated from .asymptomatic donors and *C. trachomatis* patients. Cellular immune responses were measured by standard proliferation assays and IFN-γ, as described in Example 7. Specifically, the majority of the antigens were in the form of single *E. coli* clones expressing Chlamydial antigens, although some recombinant proteins were also used in the assays. The single *E. coli* clones were titered on 1 x 10^4 monocyte-derived dendritic cells and after two hours, the culture was washed and 2.5 x 10^4 T-cells were added. The assay using the recombinant proteins were performed as previously described. Proliferation was determined after four days with a standard ^{3}H-thymidine pulse for the last 18 hours. Induction of IFN-γ was determined from culture supernatants harvested after four days using standard ELISA assays, as described above. The results show that all the *C. trachomatis* antigens tested, except for C.T. Swib, elicited a proliferative response from one or more different T-cell lines derived form *C. trachomatis* patients. In addition, proliferative responses were elicited from both the *C. trachomatis* patients and asymptomatic donors for the following *Chlamydia* genes, CT622, groEL, pmpD, CT610 and rS13.

The 12G3-83 clone also contains sequences to CT734 and CT764 in addition to CT622, and therefore these gene sequence may also have immunoreactive epitopes. Similarly, clone 21G12-60 contains sequences to the hypothetical protein genes CT229 and CT228 in addition to CT875; and 15H2-76 also contains sequences

from CT812 and CT088, as well as sharing homology to the sycE gene. Clone 11H3-61 also contains sequences sharing homology to the PGP6-D virulence protein.

Table IV.

Clone	C. t. Antigen (putative*)	TCL from Asymp. Donors	TCL from C. t. Patients	SEQ ID NO:
1B1-66 (E. coli)	Swib	2/2	0/4	5
1B1-66 (protein)	Swib	2/2	0/4	5
12G3-83 (E. coli)	CT622*	2/2	4/4	57
22B3-53 (E. coli)	groEL	1/2	4/4	111
22B3-53 (protein)	groEL	1/2	4/4	111
15H2-76 (E. coli)	PmpD*	1/2	3/4	87
11H3-61 (E. coli)	rL1*	0/2	3/4	60
14H1-4 (E. coli)	TSA	0/2	3/4	56
14H1-4 (protein)	TSA	0/2	3/4	56
11G10-46 (E. coli)	CT610	1/2	1/4	62
10C10-17 (E. coli)	rS13	1/2	1/4	62
10C10-17 (protein)	rS13	1/2	1/4	62
21G12-60 (E. coli)	CT875*	0/2	2/4	110
11H4-32 (E. coli)	dnaK	0/2	2/4	59
21C7-8 (E. coli)	dnaK	0/2	2/4	115
17C10-31 (E. coli)	CT858	0/2	2/4	114

EXAMPLE 9

PROTECTION STUDIES USING *CHLAMYDIA* ANTIGENS

1. SWIB

Protection studies were conducted in mice to determine whether immunization with chlamydial antigens can impact on the genital tract disease resulting from chlamydial inoculation. Two models were utilized; a model of intravaginal inoculation

that uses a human isolate containing a strain of *Chlamydia psittaci* (MTW447), and a model of intrauterine inoculation that involves a human isolate identified as *Chlamydia trachomatis*, serovar F (strain NI1). Both strains induce inflammation in the upper genital tract, which resemble endometritis and salpingitis caused by *Chlamydia trachomatis* in women. In the first experiment, C3H mice (4 mice per group) were immunized three times with 100 μg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5). Inoculations were at the base of the tail for systemic immunization. Two weeks after the last immunization, animals were progesterone treated and infected, either thru the vagina or by injection of the inoculum in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored (from + for very mild, to +++++ for very severe). Scores attributed to each single oviduct /ovary were summed and divided by the number of organs examined to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control-immunized animals receiving empty vector showed consistent inflammation with an ovary /oviduct mean inflammation score of 6.12, in contrast to 2.62 for the DNA-immunized group. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 8.37, versus 5.00 for the DNA-immunized group. Also, in the later model, vaccinated mice showed no signs of tubal occlusion while negative control vaccinated groups had inflammatory cells in the lumen of the oviduct

In a second experiment, C3H mice (4 mice per group) were immunized three times with 50 μg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5) encapsulated in Poly Lactide co-Glycolide microspheres (PLG); immunizations were made intra-peritoneally. Two weeks after the last immunization, animal were progesterone treated and infected by inoculation of *C. psittaci* in the vagina. Two weeks after infection, mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored as previously described. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean of inflammation for the group. Negative control-

immunized animals receiving PLG-encapsulated empty vector showed consistent infammation with an ovary /oviduct mean inflammation score of 7.28, versus 5.71 for the PLG-encapsulated DNA immunized group. Inflammation in the peritoneum was 1.75 for the vaccinated group versus 3. 75 for the control.

In a third experiment, C3H mice (4 per group) were immunized three times with 10 µg of purified recombinant protein, either SWIB (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5, or S13 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12) mixed with Cholera Toxin (CT); the preparation was administred intranasally upon anaesthesia in a 20 uL volume. Two weeks after the last immunization, animal were progesterone treated and infected, either by vaginal inoculation of *C. psittaci* or by injection of *C. trachomatis* serovar F in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. The degree of inflammation was scored as described above. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control- immunized animals receiving cholera toxin alone showed an ovary /oviduct mean inflammation score of 4.25 (only 2 mice analyzed ; 2 other died) versus 5.00 for the s13 plus cholera toxin-immunized group, and 1.00 for the SWIB plus cholera toxin. Untreated infected animals had an ovary /oviduct mean inflammation score of 7. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 7.37 versus 6.75 for the s13 plus cholera toxin-immunized group and 5.37 for the SWIB plus cholera toxin-immunized group. Untreated infected animals had an ovary /oviduct mean inflammation score of 8.

The three experiments described above suggest that SWIB-specific protection is obtainable. This protective effect is more marked in the model of homologous infection but is still present when in a heterologous challenge infection with *C. psittaci.*

2. CT529/Cap1

CT529/Cap1 was identified earlier as a product from Chlamydia that stimulates CD8+ CTL. In this example, we sought to confirm that immunization with Cap1 would be protective in an animal model of chlamydia infection.

To generate recombinant vaccinia virus for delivery of a Cap1 immunogenic fragment, a DNA fragment containing a modified Kozak sequence and base pairs 319-530 of the cap1 gene (CT529) was amplified from C. trachomatis L2 genomic DNA using PCR™ and ligated into pSC11ss (Earl PL, Koenig S, Moss B (1991) Biological and immunological properties of human immunodeficiency virus type 1 envelope glycoprotein: analysis of proteins with truncations and deletions expressed by recombinant vaccinia viruses. *J Virol.* 65:31-41). DNA digested with SalI and StuI. The portion of the cap1 gene ligated into pSC11ss encodes amino acids 107-176 of Cap1 protein, containing the previously identified CTL epitope of amino acids 139-147. The resulting plasmid was used to transfect CV-1 cells (ATCC# CCL-70; Jensen FC et al. (1964) Infection of human and simian tissue cultures with Rous Sarcoma Virus. Proc. Natl. Acad. Sci. USA 52: 53-59.) which were subsequently infected with wild-type vaccinia virus. Homologous recombination between the wild-type virus and plasmid DNA generated recombinant vaccinia viruses which were selected on the basis of both beta-galactosidase expression and the inactivation of thymidine kinase, as described previously (Chakrabarti et al, Mol Cell Biol. 1985, 5(12):3403-9). Recombinant virus was plaque purified three times and titered after growth in human TK-143B cells. Virus preparations were treated with equal volume of 0.25 mg/ml trypsin for 30 mins. at 37°C and diluted in PBS prior to immunization of mice. Groups of 5 mice were used for all experimental and control groups. The data presented below are representative of three independent experiments.

A group of mice was immunized with 10^6 of the recombinant vaccinia i.p. and was allowed to recover for 3 weeks. Negative control groups were immunized with either buffer alone or wild-type vaccinia. As a positive control, a group of mice was infected i.v. with 10^6 i.f.u. of C. trachomatis. The number of organisms given to the positive control group has been previously shown to be cleared within 2 weeks. After 3 weeks, animals in each of the groups were challenged i.v. with 10^6 i.f.u. of C.

trachomatis. Three days after challenge the mice were sacrificed and the number of i.f.u. per spleen was determined.

The mean number of organisms found in the spleens of animals immunized with the vaccinia virus expressing Cap1 ($7.1x10^4$) was 2.6-fold fewer ($p<0.01$; Wilcoxon's-Rank Sum analysis) than animals in the control groups immunized with either buffer ($1.8x10^5$) or wild-type vaccinia ($1.9x10^5$). Animals in the positive group had 77-fold fewer organisms (2.4x103) per spleen than animals in the negative control groups ($p<0.01$; Wilcoxon's-Rank Sum analysis). These data demonstrate that immunization with an immunogenic fragment of Cap1 can afford a statistically significant level of protection against C. trachomatis infection.

EXAMPLE 10

Pmp/Ra12 FUSION PROTEINS

Various Pmp/Ra12 fusion constructs were generated by first synthesizing PCR fragments of a Pmp gene using primers containing a Not I restriction site. Each PCR fragment was then ligated into the NotI restriction site of pCRX1. The pCRX1 vector contains the 6HisRa12 portion of the fusion. The Ra12 portion of the fusion construct encodes a polypeptide corresponding to amino acid residues 192-323 of *Mycobacterium tuberculosis* MTB32A, as described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference. The correct orientation of each insert was determined by its restriction enzyme pattern and its sequence was verified. Multiple fusion constructs were made for PmpA, PmpB, PmpC, PmpF and PmpH, as described further below:

PmpA Fusion Proteins

PmpA is 107 kD protein containing 982 aa and was cloned from serovar E. The PmpA protein was divided into 2 overlapping fragments, the PmpA(N-terminal) and (C-terminal) portions.

PmpA(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGTTTATAACAAAGGAACTTATG (SEQ ID NO: 306)

GAGAGCGGCCGCTTACTTAGGTGAGAAGAAGGGAGTTTC (SEQ ID NO: 307)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 308, encoding a 66 kD protein (619aa) expressing the segment 1-473 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 309.

PmpA(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCCATTCTATTCATTTCTTTGATCCTG (SEQ ID NO: 310)
GAGAGCGGCCGCTTAGAAGCCAACATAGCCTCC (SEQ ID NO: 311)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 312, encoding a 74 kD protein (691aa) expressing the segment 438-982 aa of PmpA. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 313.

PmpF Fusion Proteins

PmpF is 112 kD protein containing 1034 aa and was cloned from the serovar E. PmpF protein was divided into 2 overlapping fragments, the PmpF(N- term) and (C-term) portions.

PmpF(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGATTAAAAGAACTTCTCTATCC (SEQ ID NO: 314)

GAGAGCGGCCGCTTATAATTCTGCATCATCTTCTATGGC (SEQ ID NO: 315)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 316, encoding a 69 kD protein (646aa) expressing the segment 1-499 aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 317.

PmpF(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACATACGAACTCTGATGGG (SEQ ID NO: 318)

GAGAGCGGCCGCTTAAAAGACCAGAGCTCCTCC (SEQ ID NO: 319)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 320, encoding a 77 kD protein (715aa) expressing the segment 466-1034aa of PmpF. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 321.

PmpH Fusion Proteins

PmpH is 108 kD protein containing 1016 aa and was cloned from the serovar E. PmpH protein was divided into 2 overlapping fragments, the PmpH(N-term)and (C-term)portions.

PmpH(N-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGCCTTTTCTTTGAGATCTAC (SEQ ID NO: 322)
GAGAGCGGCCGCTTACACAGATCCATTACCGGACTG (SEQ ID NO: 323)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 324, encoding a 64 kD protein (631aa) expressing the segment 1-484 aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 325. The donor line CHH037 was found to be reactive against this protein.

PmpH(C-term) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCCTGTAGTACAAAATAATTCAGC (SEQ ID NO: 326)
GAGAGCGGCCGCTTAAAAGATTCTATTCAAGCC (SEQ ID NO: 327)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 328, encoding a 77 kD protein (715aa) expressing the segment 449-1016aa of PmpH. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 329. The patient line CT12 was found to be reactive in response to this protein.

PmpB Fusion Proteins

PmpB is 183 kD protein containing 1750 aa and was cloned from the serovar E. PmpB protein was divided into 4 overlapping fragments, PmpB(1), (2), (3) and (4).

PmpB(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATGGCTGTCAGCTACTGCG (SEQ ID NO: 330)

GAGAGCGGCCGCTTACTTAATGCGAATTTCTTCAAG (SEQ ID NO: 331)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 332, and encodes is a 53 kD protein (518aa) expressing the segment 1-372 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 333.

PmpB(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGGTGACCTCTCAATTCAATCTTC (SEQ ID NO: 334)

GAGAGCGGCCGCTTAGTTCTCTGTTACAGATAAGGAGAC (SEQ ID NO: 335)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 336 and encodes a 60 kD protein (585aa) expressing the segment 330-767 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 337. Cell lines derived from patient lines CT1, CT3, CT4 responded to this recombinant pmpB protein.

PmpB(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGACCAACTGAATATCTCTGAGAAC (SEQ ID NO: 338)

GAGCGGCCGCTTAAGAGACTACGTGGAGTTCTG (SEQ ID NO: 339)

respectively. The resulting fusion has a DNA sequence set forth in SEQ ID NO: 340 encodes a 67 kD protein (654aa) expressing the segment 732-1236 aa of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 341

PmpB(4) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGGAACTATTGTGTTCTCTTCTG (SEQ ID NO: 342)

GAGAGCGGCCGCTTAGAAGATCATGCGAGCACCGC (SEQ ID NO: 343)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 344 encodes a 76 kD protein (700aa) expressing the segment 1160-1750 of PmpB. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 345.

PmpC Fusion Proteins

PmpC is 187 kD protein containing 1774 aa and was cloned from the serovar E/L2. PmpC protein was divided into 3 overlapping fragments, PmpC(1), (2) and (3).

PmpC(1) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCATGAAATTTATGTCAGCTACTGC (SEQ ID NO: 346)

GAGAGCGGCCGCTTACCCTGTAATTCCAGTGATGGTC (SEQ ID NO: 347)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 348 and encodes a 51 kD protein (487aa) expressing the segment 1-340 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 349.

PmpC(2) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATACACAAGTATCAGAATCACC (SEQ ID NO: 350)

GAGAGCGGCCGCTTAAGAGGACGATGAGACACTCTCG (SEQ ID NO: 351)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 352 and encodes a 60 kD protein (583aa) expressing the segment 305-741 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 353.

PmpC(3) was amplified by the sense and antisense primers:

GAGAGCGGCCGCTCGATCAATCTAACGAAAACACAGACG (SEQ ID NO: 354)

GAGAGCGGCCGCTTAGACCAAAGCTCCATCAGCAAC (SEQ ID NO: 355)

respectively. The resulting fusion construct has a DNA sequence set forth in SEQ ID NO: 356 and encodes a 70 kD protein (683aa) expressing the segment 714-1250 aa of PmpC. The amino acid sequence of the fusion protein is set forth in SEQ ID NO: 357.

EXAMPE 11

IMMUNOGENICITY OF CT622

Chlamydia-specific T cells lines were generated from two patients with Chlamydia infections and the lines were designated CT1 and CT13. The T cell lines were either generated against monocyte-derived dendritic cells infected *C. trachomatis* serovar E for 72 hours (CT1-ERB) or against killed serovar E elementary bodies (EB) (CT13-EEB). Once generated, the lines were tested against the recombinant Chlamydia-specific protein, CT622 in a proliferation assay. Proliferation assays were performed by stimulating $2.5x10^4$ T cells in the presence of $1x10^4$ monocyte-derived dendritic cells with either recombinant CT antigens (2μg/ml) or Chlamydia EBs (1μg/ml). The assay was incubated for 4 days with a ^{3}H-thymidine pulse for the last 18 hours.

The cell line CT1-ERB demonstrated proliferative responses significantly above the media controls when stimulated with CT622, CT875, and CT EB. The cell line CT13-EEB demonstrated a proliferative response significantly above media controls when stimulated with CT622, CT875, and CT EB (see Figure 12).

EXAMPLE 12

CLONING AND EXPRESSION OF FULL LENGTH CHLAMYDIA TRACHOMATIS GENES CT611, ORF3 AND OppA1

Recombinant protein expression of the full-length open reading frames was performed for clones containing genes CT611, ORF-3, and oppA1. The elones that contained the genes of interest were CtL2-8 (SEQ ID NO:285) which encoded 4 ORFs (CT474, CT473, CT060, and CT139), CtL2-10 (SEQ ID NO:284) which encoded the ORFs of CT610 and CT611, and clones 16CtL2-16 (SEQ ID NO:47), 16-D4-22 (SEQ ID NO:119) and 19-A5-54 (SEQ ID NO:84) which all contained sequences related to ORF-3. Sequences within CtL2-10 (Ct-610) and CtL2-16 (ORF-3) were also independently identified by the T-cell expression cloning approach. The clone CtL2-8 was further investigated as this clone had stimulated the proliferative responses and IFN-gamma production by two T cell lines generated against serovar E.

Cloning and expression of clone sequences:

CtL2-10 was found to encode two open reading frames (ORFs), CT610 and CT611, and these were found organized adjacent to each other within the genomic clone. The full length ORF of CT610 (containing a PQQ synthesis domain) was previously expressed and demonstrated to stimulate the proliferative responses of T cell lines generated against Chlamydia. To determine whether the second ORF, CT611, was also recognized by T cells, the full-length sequence of CT611 was PCR amplified and engineered for protein expression. The nucleotide sequence is disclosed in SEQ ID NO:361 with the corresponding amino acid sequence disclosed in SEQ ID NO:365.

The second serological clone, CtL2-8, was found to contain 4 ORFs (CT474, CT473, CT060, and CT139). Overlapping peptides to the three smallest predicted ORFs (CT474, CT473, and CT060) did not stimulate the proliferative responses of T

cell lines. This suggested that the immunostimulatory antigen resides in the fourth ORF, CT139. The ORF of CT139 is approximately 450 nucleotides. The full-length nucleotide sequence is disclosed in SEQ ID NO:359 and the full-length amino acid sequence is disclosed in SEQ ID NO:363. Amino acid sequence comparison from Genbank revealed that it is an oligo-peptide binding protein (oppA1) as well as belonging to the peptide ABC transporter family. This protein is 462 amino acids long with a predicted size of 48.3kDa and appears to contain 2 trans-membrane regions.

To express the full-length sequence of oppA1, oligonucleotides were designed which specifically amplified sequences starting from amino acid residue 22 (devoid of the first transmembrane domain), the nucleotide sequence for which is disclosed in SEQ ID NO:358 and, the amino acid sequence of which is disclosed in SEQ ID NO:362. This was shown to express the protein in E. coli.

The full-length cloning and recombinant protein expression of ORF-3 was also achieved. The nucleotide and amino acid sequences are disclosed in SEQ ID NOs:360 and 364, respectively.

EXAMPLE 13

RECOMBINANT CHLAMYDIAL ANTIGENS RECOGNIZED BY T CELL LINES

Patient T cell lines were generated from the following donors: CT1, CT2, CT3, CT4, CT5, CT6, CT7, CT8, CT9, CT10, CT11, CT12, CT13, CT14, CT15, and CT16, some of which were discussed above. A summary of their details is included in Table V.

Table V: C. *trachomatis* patients

Patients	**Gender**	Age	**Clinical Manifestation**	**Serovar**	**IgG titer**	**Multiple Infections**
CT1	M	27	NGU	LCR	Negative	No
CT2	M	24	NGU	D	Negative	E
CT3	M	43	Asymptomatic	J	Ct 1:512	No

			Shed Eb Dx was HPV		Cp 1:1024 Cps 1:256	
CT4	F	25	Asymptomatic Shed Eb	J	Ct 1:1024	Y
CT5	F	27	BV	LCR	Ct 1:256 Cp 1:256	F/F
CT6	M	26	Perinial rash Discharge, dysuria	G	Cp 1:1024	N
CT7	F	29	BV Genital ulcer	E	Ct 1:512 Cp 1:1024	N
CT8	F	24	Not Known	LCR	Not tested	NA
CT9	M	24	asymptomatic	LCR	Ct 1:128 Cp 1:128	N
CT10	F	20	Mild itch vulvar	negative	negative	12/1/98
CT11	F	21	BV Abnormal pap smear	J	Ct 1:512	F/F/J/E/E PID 6/96
CT12	M	20	asymptomatic	LCR	Cp 1:512	N
CT13	F	18	BV, gonorrhea, Ct vaginal discharge, dysuria	G	Ct 1:1024	N
CT14	M	24	NGU	LCR	Ct 1:256	N

					Cp 1:256	
CT15	F	21	Muco-purulint cervicitis Vaginal discharge	culture	Ct 1:256 Ct IgM 1:320 Cp 1:64	N
CT16	M	26	Asymptomatic/ contact	LCR	NA	N
CL8	M	38	No clinical history of disease	negative	negative	N

NGU=Non-Gonococcal Urethritis; BV=Bacterial Vaginosis; CT=Chlamydia trachomatis; Cp=Chlamydia pneumoniae; Eb=Chlamydia elementary bodies; HPV=human papiloma virus; Dx=diagnosis; PID=pelvic inflammatory disease; LCR=Ligase chain reaction.

PBMC were collected from a second series of donors and T cell lines have been generated from a sub-set of these. A summary of the details for three such T cell lines is listed in the table below.

Table III: Normal Donors				
Donor	**Gender**	**Age**	**CT IgG Titer**	**CP IgG Titer**
CHH011	F	49	1:64	1:16
CHH037	F	22	0	0
CHH042	F	25	0	1:16

Donor CHH011 is a heathly 49 year old female donor sero-negaitve for *C. trachomatis*. PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. Donor CHH037 is a 22 year old healthy

female donor sero-negative for C. trachomatis. PBMC poruced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response. CHH042 is a 25 year old healthy female donor with an IgG titer of 1:16 to *C. pneumoniae*. PBMC produced higher quantities of IFN-gamma in response to *C. trachomatis* elementary bodies as compared to *C. pneumoniae* elementary bodies, indicating a *C. trachomatis*-specific response.

Recombinant proteins for several *Chlamydia trachomatis* genes were generated as described above. Sequences for MOMP was derived from serovar F. The genes CT875, CT622, pmp-B-2, pmpA, and CT529 were derived from serovar E and sequences for the genes gro-EL, Swib, pmpD, pmpG, TSA, CT610, pmpC, pmpE, S13, lpdA, pmpI, and pmpH-C were derived from LII.

Several of the patient and donor lines described above were tested against the recombinant Chlamydia proteins. Table IV summarizes the results of the T cell responses to these recombinant Chlamydia proteins.

Table VII: Recombinant Chlamydia Antigens Recognized By T Cell Lines

Antigen	Sero-var	#of hits	C L8 L2	CT 10 E	CT1 E	CT3 E	CT4 L2	CT5 E	CT 11 E	CT 12 E	CT 13 E	CH H-011 E	CH H-037 E
gro-EL (CT110)	L2	10	-	+	+	+	+	+	+	+	+	+	+
MompF (CT681)	F	10	-	+	+	+	+	+	+	+	+	+	+
CT875	E	8	-	+	+	-	+	+	+	+	+	-	+
SWIB (CT460)	L2	8	+	+	-	+	-	+	-	+	+	+	+
pmpD (CT812)	L2	5	-	+	+	+	+	-	-	+	+	-	-

pmpG (CT871)	L2	6	-	+	+	-	+	+	nt	-	+	+	-
TSA (CT603)	L2	6	-	-	+	+	+	+	-	-	+	-	+
CT622	E	3	-	-	+	-	+	-	-	-	+	-	-
CT610	L2	3	-	+	-	+	-	-	-	+	-	-	-
pmpB-2 (CT413)	E	3	-	-	+	+	+	-	-	-	-	-	-
pmpC (CT414)	L2	4	-	-	-	+	-	+	-	+	-	-	+
pmpE (CT869)	L2	3	-	+	+	-	-	-	-	-	+	-	-
S13 (CT509)	L2	2	+	-	-	-	+	-	-	-	-	-	-
lpdA (CT557)	L2	3	-	-	+	+	-	-	-	-	-	+	-
pmpI (CT874)	L2	2	-	-	+	-	-	-	-	-	-	+	-
pmpH-C (CT872)	L2	1	-	-	-	-	-	-	-	+	-	-	-
pmpA (CT412)	E	0	-	-	-	-	-	-	-	-	-	-	-
CT529	E	0	-	-	-	-	-	-	-	-	-	-	-

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

Claims

What is Claimed:

1. A composition for eliciting an immune response comprising a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.

2. The composition of claim 1, wherein the immunogenic fragment comprises at least a CTL epitope consisting essentially of amino acids 139-147 of a Cap1 protein.

3. The composition of claim 1, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.

4. The composition of claim 1, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

5. The composition of claim 1, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.

6. The composition of claim 5, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

7. The composition of claim 1, wherein the immunogenic fragment is

immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

8. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to an animal an effective amount of a composition according to claim 1.

9. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal an effective amount of a composition according to claim 1.

10. A composition for eliciting an immune response comprising an isolated polynucleotide that encodes a Chlamydia Cap1 protein or an immunogenic fragment thereof and an immunostimulant.

11. The composition of claim 10, wherein the immunogenic fragment comprises at least the CTL epitope sequence consisting essentially of amino acids 139-147 of a Cap1 protein.

12. The composition of claim 10, wherein the Cap 1 protein comprises an amino acid sequence set forth in SEQ ID NO: 121 or a sequence having at least about 90% identity to the sequence set forth in SEQ ID NO: 121.

13. The composition of claim 10, wherein the Cap1 protein or immunogenic fragment thereof comprises a sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

14. The composition of claim 10, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein.

15. The composition of claim 14, wherein the immunogenic fragment comprises amino acids 107-176 of a Cap1 protein having an amino acid sequence set forth in any one of SEQ ID NOs: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139.

16. The composition of claim 10, wherein the immunogenic fragment is immunologically reactive with a CD8+ T-cell of a Chlamydia-infected animal.

17. The composition of claim 10, wherein the isolated polynucleotide is operably linked within a viral delivery vector.

18. The composition of claim 17, wherein the viral delivery vector is a vaccinia virus delivery vector.

19. A method for stimulating a Chlamydia-specific T-cell response in an animal comprising administering to said animal an effective amount of a composition according to claim 10.

20. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to an animal said effective amount of a composition according to claim 10.

21. A method for inhibiting the development of a Chlamydia infection in an animal, comprising administering to said animal an effective amount of a composition according to claim 18.

22. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO:358-361;

(b) complements of the sequences provided in SEQ ID NO:358-361;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:358-361;

(d) sequences that hybridize to a sequence provided in SEQ ID NO:358-361, under highly stringent conditions;

(e) sequences having at least 95% identity to a sequence of SEQ ID NO:358-361;

(f) sequences having at least 99% identity to a sequence of SEQ ID NO:358-361; and

(g) degenerate variants of a sequence provided in SEQ ID NO:358-361.

23. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences encoded by a polynucleotide of claim 22;

(b) sequences having at least 95% identity to a sequence encoded by a polynucleotide of claim 22; and

(c) sequences having at least 99% identity to a sequence encoded by a polynucleotide of claim 22.

24. An isolated polypeptide comprising at least an immunogenic fragment of a polypeptide sequence selected from the group consisting of:

(a) a polypeptide sequence set forth in SEQ ID NO:362-365,

(b) a polypeptide sequence having at least 95% identity with a sequence set forth in SEQ ID NO:362-365, and

(c) a polypeptide sequence having at least 99% identity with a sequence set forth in SEQ ID NO:362-365.

25. An expression vector comprising a polynucleotide of claim 22 operably linked to an expression control sequence.

26. A host cell transformed or transfected with an expression vector according to claim 25.

27. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of any one of claims 23 and 24.

28. A method for detecting the presence of Chlamydia in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with a binding agent that binds to a polypeptide of any one of claims 23 and 24;

(c) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of Chlamydia in the patient.

29. A fusion protein comprising at least one polypeptide according to claim 23 or claim 24.

30. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 358-361 under highly stringent conditions.

31. A method for stimulating and/or expanding T cells specific for a Chlamydia protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) a polypeptide according to claim 23 or claim 24;

(b) a polynucleotide according to claim 22; and

(c) an antigen-presenting cell that expresses a polynucleotide according to claim 22,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

32. An isolated T cell population, comprising T cells prepared according to the method of claim 31.

33. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

(a) a polypeptide according to claim 23 or claim 24;

(b) a polynucleotide according to claim 22;

(c) an antibody according to claim 27;

(d) a fusion protein according to claim 29;

(e) a T cell population according to claim 32; and

(f) an antigen presenting cell that expresses a polypeptide according to claim 23 or claim 24.

34. A method for stimulating an immune response in a patient, comprising administering to the patient a composition selected from the group consisting of;

(a) a composition of claim 33;

(b) a polynucleotide sequence of any one of SEQ ID NO:407-430, 525-559, and 582-598; and

(c) a polypeptide sequence of any one of SEQ ID NO:431-454 and 560-581.

35. A method for the treatment of Chlamydia infection in a patient, comprising administering to the patient a composition seleeted from the group consisting of;

(a) a composition of claim 33;

(b) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559, and 582-598; and

(d) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581.

36. A method for determining the presence of Chlamydia in a patient, comprising the steps of:

(a) obtaining a biological sample from the patient;

(b) contacting the biological sample with an oligonucleotide according to claim 30;

(c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(d) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefore determining the presence of the cancer in the patient.

37. A diagnostic kit comprising at least one oligonucleotide according to claim 30.

38. A diagnostic kit comprising at least one antibody according to claim 27 and a detection reagent, wherein the detection reagent comprises a reporter group.

39. A method for the treatment of Chlamydia in a patient, comprising the steps of:

(a) incubating CD4+ and/or CD8+ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to any one of claims 23 and 24;

(ii) a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581;

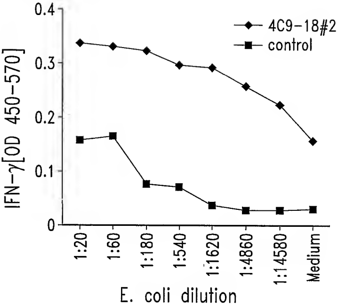
(iii) a polynucleotide according to claim 22;

(iv) a polynucleotide sequence of any one of SEQ ID NO: 407-430, 525-559 and 582-598;

(v) an antigen presenting cell that expresses a polypeptide sequence set forth in any one of claims 23 and 24;

(vi) an antigen presenting cell that expresses a polypeptide sequence of any one of SEQ ID NO: 431-454 and 560-581, such that the T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells.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0.2
0.1
0
IFN-γ[OD 450-570]
4C9-18#2
control
1:20
1:60
1:180
1:540
1:1620
1:4860
1:14580
Medium
E. coli dilution

Fig. 1

2/11

Retroviral vector pBIB-KS — LTR — KS-MCS | IRES-Blasto^r — LTR —

```
        Kozak-Start
 GA TCT GCC GCC ACC ATG GAA TTC GAT ATC GGA TCC CTG CAG
      A CGG CGG TGG TAC CTT AAG CTA TAG CCT AGG GAC GTC
(BglII)                   EcoRI          BamHI   PstI

AAG CTT GAG CTC GAG CGC GGC CGC TAA TTA GCT GAG
TTC GAA CTC GAG CTC GCG CCG GCG ATT AAT CGA CTC AGC T
HinDIII      XhoI        NotI   Stop Stop Stop (SalI)
```

ReadingFrame 1
KS1+

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      A CGG CGG TGG TAC CCT TAA GCT ATA GCC TAG GGA CGT C
(BglII)                    EcoRI          BamHI   PstI

AA GCT TGA GCT CGA GCG CGG CCG CTA ATT AGC TGA G
TT CGA ACT CGA GCT CGC GCC GGC GAT TAA TCG ACT CAG CT
HinDIII     XhoI         NotI    Stop Stop Stop (SalI)
```

ReadingFrame 1
KS2+

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(BglII)                    EcoRI          BamHI   PstI

A AGC TTG AGC TCG AGC GCG GCC GCT AAT TAG CTG AG
T TCG AAC TCG AGC TCG CGC CGG CGA TTA ATC GAC TCA GCT
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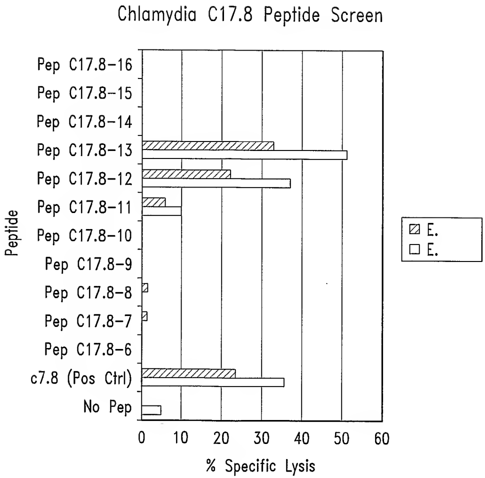
ReadingFrame 3
KS3+

Fig. 2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Peptide
Pep C17.8-16
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Pep C17.8-13
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Pep C17.8-11
Pep C17.8-10
Pep C17.8-9
Pep C17.8-8
Pep C17.8-7
Pep C17.8-6
c7.8 (Pos Ctrl)
No Pep
0
10
20
30
40
50
60
% Specific Lysis
E.
E.

Fig. 3

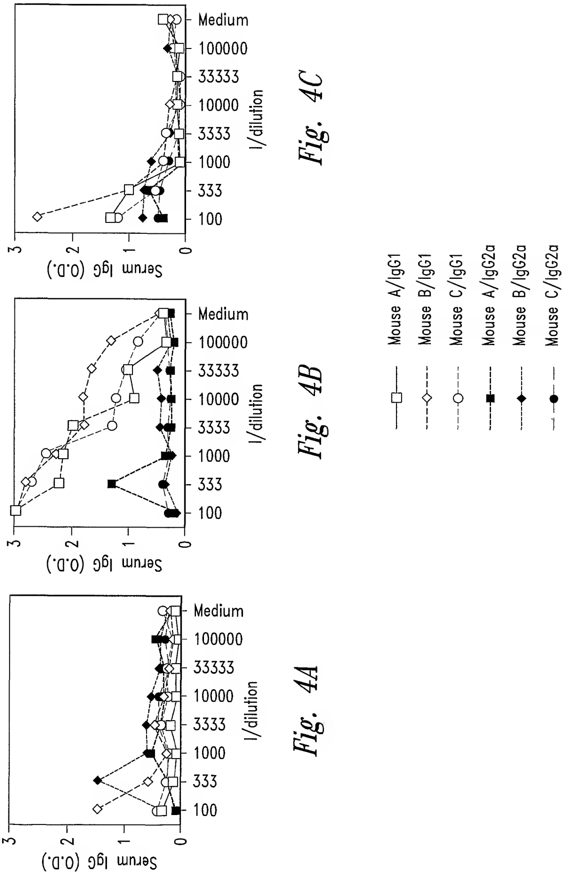
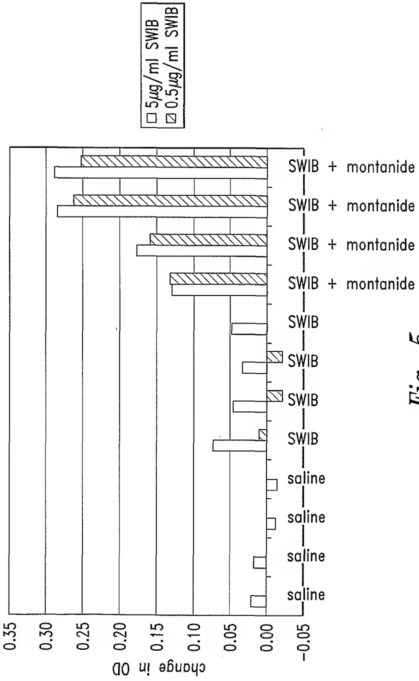


Fig. 4A

Fig. 4B

Fig. 4C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0.5μg/ml SWIB
SWIB + montanide
SWIB + montanide
SWIB + montanide
SWIB + montanide
SWIB
SWIB
SWIB
SWIB
saline
saline
saline
saline
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
-0.05
change in OD

Fig. 5

CP SWIB Nde (5' primer)
5' GATATACATATGCATCACCATCACCATCACATGAGTCAAAAAAATAAAAACTCT

CP SWIB EcoRI (3' primer)
5' CTCGAGGAATTCTTATTTTACAATATGTTTGGA

CP S13 Nde (5' primer)
5' GATATACATATGCATCACCATCACCATCACATGCCACGCATCATTGGAATGAT

CP S13 EcoRI (3' primer)
5' CTCGAGGAATTCTTATTTCTTCTTACCTGC

Fig. 6

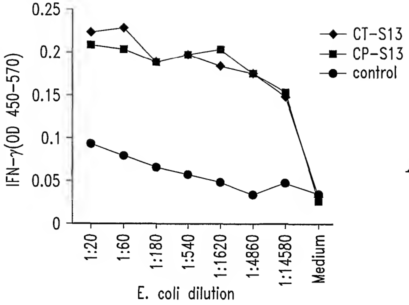
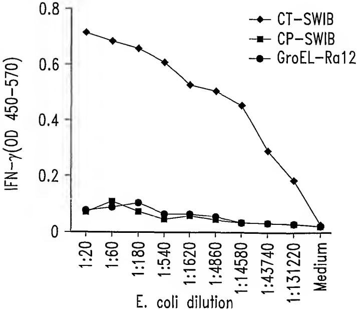

0.25
0.2
0.15
0.1
0.05
0
IFN-γ(OD 450-570)
CT-S13
CP-S13
control
1:20
1:60
1:180
1:540
1:1620
1:4860
1:14580
Medium
E. coli dilution

Fig. 7A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0.6
0.4
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0
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CP-SWIB
GroEL-Ra12
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1:1620
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1:131220
Medium
E. coli dilution

Fig. 7B

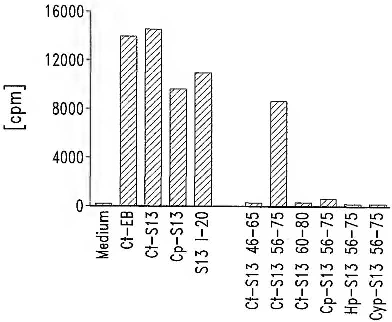
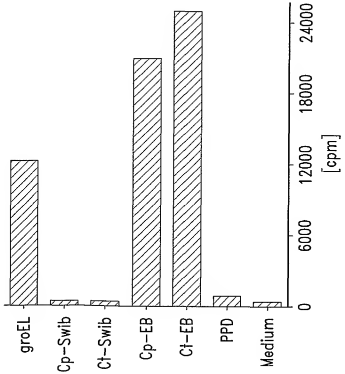

16000
12000
8000
4000
0
[cpm]
Medium
Ct-EB
Ct-S13
Cp-S13
S13 1-20
Ct-S13 46-65
Ct-S13 56-75
Ct-S13 60-80
Cp-S13 56-75
Hp-S13 56-75
Cyp-S13 56-75

Fig. 8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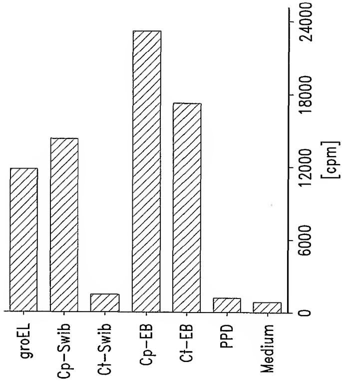
Cp-Swib
Ct-Swib
Cp-EB
Ct-EB
PPD
Medium
0
6000
12000
18000
24000
[cpm]

Fig. 9A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Ct-EB
PPD
Medium
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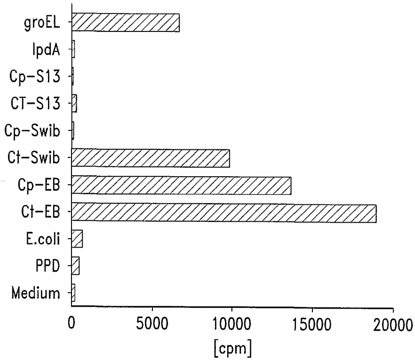
6000
12000
18000
24000
[cpm]

Fig. 9B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lpdA
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CT-S13
Cp-Swib
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Ct-EB
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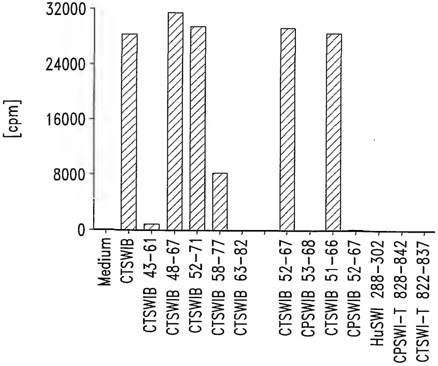
20000
[cpm]

Fig. 10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[cpm]
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CTSWIB 43-61
CTSWIB 48-67
CTSWIB 52-71
CTSWIB 58-77
CTSWIB 63-82
CTSWIB 52-67
CPSWIB 53-68
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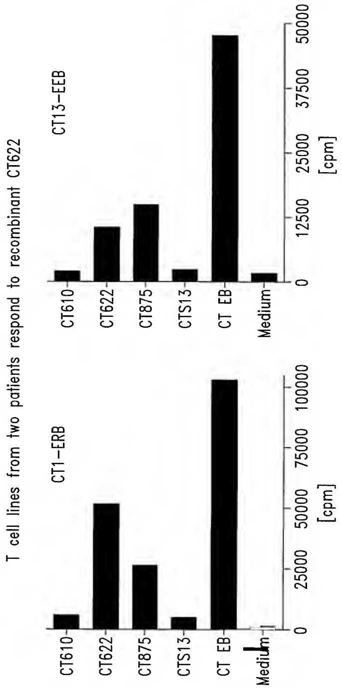
CPSWIB 52-67
HuSWI 288-302
CPSWI-T 828-842
CTSWI-T 822-837

Fig. 11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CT610
CT622
CT875
CTS13
CT EB
Medium
0
25000
50000
75000
100000
[cpm]
CT13-EEB
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CT622
CT875
CTS13
CT EB
Medium
0
12500
25000
37500
50000
[cpm]

Fig. 12

SEQUENCE LISTING

<110> Corixa Corporation
Fling, Steven P.
Skeiky, Yasir A. W.
Probst, Peter
Bhatia, Ajay

<120> COMPOUNDS AND METHODS FOR TREATMENT AND
DIAGNOSIS OF CHLAMYDIAL INFECTION

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Ile Ile Lys Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp
        35                  40                  45
Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val
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            20                  25                  30
Gln Ser His Arg
        35
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50 55 60
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Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
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Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
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Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
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50 55 60
Ile Leu Trp Arg Leu Thr Met Gln Arg Leu Trp Trp Val Leu Asp Ser
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Met His Ser Ser Leu Cys Ser Arg Ser Phe Trp Asn Ala Leu Pro Thr
130 135 140
Phe Ser Asn Trp Cys Arg Cys Leu Leu Gln Trp Val Phe Val Arg Leu
145 150 155 160
Trp Leu Leu Asp Val Arg Ser Leu Leu Gln Leu Leu Asp Cys Ala Leu
165 170 175
Ser Ala Pro Glu His Lys Gly Phe Phe Lys Phe Leu Lys Lys Lys Ala
180 185 190
Val Ser Lys Lys Lys Gln Pro Phe Leu Ser Thr Lys Cys Leu Ala Phe
195 200 205
Leu Ile Val Lys Ile Val Phe Leu
210 215

<210> 21
<211> 1256
<212> DNA
<213> Chlamydia trachomatis

<400> 21
ctcgtgccgg cacgagcaaa gaaatccctc aaaaaatggc cattattggc ggtggtgtga 60
tcggttgcga attcgcttcc ttattccata cgttaggctc cgaagtttct gtgatcgaag 120
caagctctca aatccttgct ttgaataatc cagatatttc aaaaaccatg ttcgataaat 180
tcacccgaca aggactccgt ttcgtactag aagcctctgt atcaaatatt gaggatatag 240
gagatcgcgt tcggttaact atcaatggga atgtcgaaga atacgattac gttctcgtat 300
ctataggacg ccgtttgaat acagaaaata ttggcttgga taaagctggt gttatttgtg 360
atgaacgcgg agtcatccct accgatgcca caatgcgcac aaacgtacct aacatttatg 420
ctattggaga tatcacagga aaatggcaac ttgcccatgt agcttctcat caaggaatca 480
ttgcagcacg gaatataggt ggccataaag aggaaatcga ttactctgct gtcccttctg 540
tgatctttac cttccctgaa gtcgcttcag taggcctctc cccaacagca gctcaacaac 600
atctccttct tcgcttactt tttctgaaaa atttgataca gaagaagaat tcctcgcaca 660
cttgcgagga ggagggcgtc tggaagacca gttgaattta gctaagtttt ctgagcgttt 720
tgattctttg cgagaattat ccgctaagct tggttacgat agcgatggag agactgggga 780
tttcttcaac gaggagtacg acgacgaaga agaggaaatc aaaccgaaga aaactacgaa 840
acgtggacgt aagaagagcc gttcataagc cttgctttta aggtttggta gttttacttc 900
tctaaaatcc aaatggttgc tgtgccaaaa agtagtttgc gtttccggat agggcgtaaa 960

tgcgctgcat gaaagattgc ttcgagagcg gcatcgcgtg ggagatcccg gatactttct 1020
ttcagatacg aataagcata gctgttccca gaataaaaac ggccgacgct aggaacaaca 1080
agatttagat agagcttgtg tagcaggtaa actgggttat atgttgctgg gcgtgttagt 1140
tctagaatac ccaagtgtcc tccaggttgt aatactcgat acacttccct aagagcctct 1200
aatggatagg ataagttccg taatccatag gccatagaag ctaaacgaaa cgtatt 1256

<210> 22
<211> 601
<212> DNA
<213> Chlamydia trachomatis

<400> 22
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tcggttgcga attcgcttcc ttattccata cgttaggctc cgaagtttct gtgatcgaag 120
caagctctca aatccttgct ttgaataatc cagatatttc aaaaaccatg ttcgataaat 180
tcacccgaca aggactccgt ttcgtactag aagcctctgt atcaaatatt gaggatatag 240
gagatcgcgt tcggttaact atcaatggga atgtcgaaga atacgattac gttctcgtat 300
ctataggacg ccgtttgaat acagaaaata ttggcttgga taaagctggt gttatttgtg 360
atgaacgcgg agtcatccct accgatgcca caatgcgcac aaacgtacct aacatttatg 420
ctattggaga tatcacagga aaatggcaac ttgcccatgt agcttctcat caaggaatca 480
ttgcagcacg gaatataggt ggccataaag aggaaatcga ttactctgct gtcccttctg 540
tgatctttac cttccctgaa gtcgcttcag taggcctctc cccaacagca gctcaacaac 600
a 601

<210> 23
<211> 270
<212> DNA
<213> Chlamydia trachomatis

<400> 23
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cacttgcgag gaggagggcg tctggaagac cagttgaatt tagctaagtt ttctgagcgt 120
tttgattctt tgcgagaatt atccgctaag cttggttacg atagcgatgg agagactggg 180
gatttcttca acgaggagta cgacgacgaa gaagaggaaa tcaaaccgaa gaaaactacg 240
aaacgtggac gtaagaagag ccgttcataa 270

<210> 24
<211> 363
<212> DNA
<213> Chlamydia trachomatis

<400> 24
ttacttctct aaaatccaaa tggttgctgt gccaaaaagt agtttgcgtt tccggatagg 60
gcgtaaatgc gctgcatgaa agattgcttc gagagcggca tcgcgtggga gatcccggat 120
actttctttc agatacgaat aagcatagct gttcccagaa taaaaacggc cgacgctagg 180
aacaacaaga tttagataga gcttgtgtag caggtaaact gggttatatg ttgctgggcg 240
tgttagttct agaataccca agtgtcctcc aggttgtaat actcgataca cttccctaag 300
agcctctaat ggataggata agttccgtaa tccataggcc atagaagcta aacgaaacgt 360
att 363

<210> 25
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<400> 25
gctcgtgccg gcacgagcaa agaaatccct caaaaaatgg ccattattgg cggtggtgtg 60
atcggttgcg aattcgcttc cttattccat acgttaggct ccgaagtttc tgtgatcgaa 120
gcaagctctc aaatccttgc tttgaataat ccagatattt caaaaaccat gttcgataaa 180
ttcacccgac aaggactccg tttcgtacta gaagcctctg tatcaaatat tgaggatata 240
ggagatcgcg ttcggttaac tatcaatggg aatgtcgaag aatacgatta cgttctcgta 300

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tctataggac gccgtttgaa tacagaaaat attggcttgg ataaagctgg tgttatttgt     360
gatgaacgcg gagtcatccc taccgatgcc acaatgcgca caaacgtacc taacatttat     420
gctattggag atatcacagg aaaatggcaa cttgcccatg tagcttctca tcaaggaatc     480
attgcagcac ggaatatagg tggccataaa gaggaaatcg attactctgc tgtcccttct     540
gtgatcttta ccttccctga agtcgcttca gtaggcctct ccccaacagc agctcaacaa     600
catctccttc ttcgcttact ttttctgaaa aatttgatac agaagaagaa ttcctcgcac     660
acttgcgagg aggagggcgt ctggaagacc agttga                               696
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<210> 26
<211> 231
<212> PRT
<213> Chlamydia trachomatis

<400> 26

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Ala Arg Ala Gly Thr Ser Lys Glu Ile Pro Gln Lys Met Ala Ile Ile
1               5                   10                  15
Gly Gly Gly Val Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu
            20                  25                  30
Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu
        35                  40                  45
Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln
    50                  55                  60
Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile
65                  70                  75                  80
Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp
                85                  90                  95
Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly
            100                 105                 110
Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr
        115                 120                 125
Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp
    130                 135                 140
Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile
145                 150                 155                 160
Ile Ala Ala Arg Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser
                165                 170                 175
Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly
            180                 185                 190
Leu Ser Pro Thr Ala Ala Gln Gln His Leu Leu Leu Arg Leu Leu Phe
        195                 200                 205
Leu Lys Asn Leu Ile Gln Lys Lys Asn Ser Ser His Thr Cys Glu Glu
    210                 215                 220
Glu Gly Val Trp Lys Thr Ser
225                 230
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<210> 27
<211> 264
<212> DNA
<213> Chlamydia pneumoniae

<400> 27

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atgagtcaaa aaaataaaaa ctctgctttt atgcatcccg tgaatatttc cacagattta      60
gcagttatag ttggcaaggg acctatgccc agaaccgaaa ttgtaaagaa agtttgggaa     120
tacattaaaa aacacaactg tcaggatcaa aaaaataaac gtaatatcct tcccgatgcg     180
aatcttgcca aagtctttgg ctctagtgat cctatcgaca tgttccaaat gaccaaagcc     240
ctttccaaac atattgtaaa ataa                                            264
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<210> 28
<211> 87
<212> PRT
<213> Chlamydia pneumoniae

<400> 28
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile
1 5 10 15
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr
20 25 30
Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln
35 40 45
Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys
50 55 60
Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala
65 70 75 80
Leu Ser Lys His Ile Val Lys
85

<210> 29
<211> 369
<212> DNA
<213> Chlamydia pneumoniae

<400> 29
atgccacgca tcattggaat tgatattcct gcaaagaaaa agttaaaaat aagtctgaca 60
tatatttatg gaataggatc agctcgttct gatgaaatca ttaaaaagtt gaagttagat 120
cctgaggcaa gagcctctga attaactgaa gaagaagtag gacgactgaa ctctctgcta 180
caatcagaat ataccgtaga aggggatttg cgacgtcgtg ttcaatcgga tatcaaaaga 240
ttgatcgcca tccattctta tcgaggtcag agacatagac tttctttacc agtaagagga 300
caacgtacaa aaactaattc tcgtactcga aaaggtaaaa gaaaaacagt cgcaggtaag 360
aagaaataa 369

<210> 30
<211> 122
<212> PRT
<213> Chlamydia pneumoniae

<400> 30
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
1 5 10 15
Ile Ser Leu Thr Tyr Ile Tyr Gly Ile Gly Ser Ala Arg Ser Asp Glu
20 25 30
Ile Ile Lys Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu
35 40 45
Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr
50 55 60
Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg
65 70 75 80
Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu
85 90 95
Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly
100 105 110
Lys Arg Lys Thr Val Ala Gly Lys Lys Lys
115 120

<210> 31
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 31

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Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1               5                  10

      <210> 32
      <211> 53
      <212> PRT
      <213> Chlamydia trachomatis

      <400> 32
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe
 1               5                  10                  15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
            20                  25                  30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr
        35                  40                  45
Lys Ala Asn Met Gly
    50

      <210> 33
      <211> 161
      <212> DNA
      <213> Chlamydia trachomatis

      <400> 33
atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc atcggaggaa      60
ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac aaaatgctgg     120
caaaaccgtt tctttcttcc caaactaaag caaatatggg a                         161

      <210> 34
      <211> 53
      <212> PRT
      <213> Chlamydia trachomatis

      <400> 34
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile
 1               5                  10                  15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
            20                  25                  30
Leu Phe Val Asn Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr
        35                  40                  45
Lys Ala Asn Met Gly
    50

      <210> 35
      <211> 55
      <212> DNA
      <213> Chlamydia pneumoniae

      <400> 35
gatatacata tgcatcacca tcaccatcac atgagtcaaa aaaaataaaa actct           55

      <210> 36
      <211> 33
      <212> DNA
      <213> Chlamydia pneumoniae

      <400> 36
ctcgaggaat tcttatttta caatatgttt gga                                    33

      <210> 37
      <211> 53
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<212> DNA
<213> Chlamydia pneumoniae

<400> 37
gatatacata tgcatcacca tcaccatcac atgccacgca tcattggaat gat 53

<210> 38
<211> 30
<212> DNA
<213> Chlamydia pneumoniae

<400> 38
ctcgaggaat tcttatttct tcttacctgc 30

<210> 39
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 39
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1 5 10 15

<210> 40
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 40
Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser
1 5 10 15

<210> 41
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 41
Lys Glu Tyr Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp
1 5 10 15

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> made in the lab

<400> 42
Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln Gly Val Ile Gly Ala

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1               5                   10                  15

     <210> 43
     <211> 15
     <212> PRT
     <213> Artificial Sequence

     <220>
     <223> made in the lab

     <400> 43
Lys Lys Leu Leu Val Pro Asp Asn Asn Leu Ala Thr Ile Ile Gly
1               5                   10                  15

     <210> 44
     <211> 509
     <212> DNA
     <213> Chlamydia

     <400> 44
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taccgtacgt gagattgctg tacaagtagc tgttatgtat ggttctagtt gcttactgcg 120
cgccgtgggc gatttagcga aaaatgattc ttctattcaa gtacgcatca ctgcttatcg 180
tgctgcagcc gtgttggaga tacaagatct tgtgcctcat ttacgagttg tagtccaaaa 240
tacacaatta gatggaacgg aaagaagaga agcttggaga tctttatgtg ttcttactcg 300
gcctcatagt ggtgtattaa ctggcataga tcaagcttta atgacctgtg agatgttaaa 360
ggaatatcct gaaaagtgta cggaagaaca gattcgtaca ttattggctg cagatcatcc 420
agaagtgcag gtagctactt tacagatcat tctgagagga ggtagagtat tccggtcatc 480
ttctataatg gaatcggttc tcgtgccgg                                   509

     <210> 45
     <211> 481
     <212> DNA
     <213> Chlamydia

     <220>
     <221> misc_feature
     <222> 23
     <223> n=A,T,C or G

     <400> 45
gatccgaatt cggcacgagg cantatttac tcccaacatt acggttccaa ataagcgata 60
aggtcttcta ataaggaagt taatgtaaga ggcttttta ttgcttttcg taaggtagta 120
ttgcaaccgc acgcgattga atgatacgca agccatttcc atcatggaaa agaacccttg 180
gacaaaaata caaaggaggt tcactcctaa ccagaaaaag ggagagttag tttccatggg 240
ttttccttat atacacccgt ttcacacaat taggagccgc gtctagtatt tggaatacaa 300
attgtcccca agcgaatttt gttcctgttt cagggatttc tcctaattgt tctgtcagcc 360
atccgcctat ggtaacgcaa ttagctgtag taggaagatc aactccaaac aggtcataga 420
aatcagaaag ctcataggtg cctgcagcaa taacaacatt cttgtctgag tgagcgaatt 480
g                                                                 481

     <210> 46
     <211> 427
     <212> DNA
     <213> Chlamydia

     <220>
     <221> misc_feature
     <222> 20
     <223> n=A,T,C or G
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<400> 46
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ataacacaga tcaaagaacg gccattcagt ttaggctctg actcaacaaa acctatgtcc 120
tctaagccct gacacattct ttgaacaacc ttatgcccgt gttcgggata agccaactct 180
cgccccccgaa acatacaaga aacctttact ttatttcctt tctcaataaa ggctctagct 240
tgctttgctt tcgtaagaaa gtcgttatca tcgatattag gcttaagctt aacctctttg 300
atacgcactt ggtgctgtgc tttcttacta tctttttctt ttttagttat gtcgtaacga 360
tacttcccgt agtccatgat tttgcacaca ggaggctctg agtttgaagc aacctcgtgc 420
cgaattc 427

<210> 47
<211> 600
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 522
<223> n=A,T,C or G

<400> 47
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cagcttattc tagaaaagtt gggagatcaa attcttggtg gaattgctga tactattgtt 120
gatagtacag tccaagatat tttagacaaa atcacaacag acccttctct aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcactccc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacacccaaa 300
agctctggga gcatgttctt agtctcagca gatattattg catcaagaat ggaaggcggc 360
gttgttctag ctttggtacg agaaggtgat tctaagccct acgcgattag ttatggatac 420
tcatcaggcg ttcctaattt atgtagtcta agaaccagaa ttattaatac aggattgact 480
ccgacaacgt attcattacg tgtaggcggt ttagaaagcg gngtggtatg ggttaatgcc 540
ctttctaatg gcaatgatat tttaggaata acaaatcttc taatgtatct tttttggagg 600

<210> 48
<211> 600
<212> DNA
<213> Chlamydia

<400> 48
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atgatgcagg aattaggtcc acactatctt tttttgtttc gcaaatgatt gattttaaat 120
cgtttgatgt gtatactatg tcgtgtaagc ctttttggtt acttctgaca ctagcccccca 180
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attgggccaa gttgcatccc acgtttagag aaagtgttgt ttttccagtt cctcccttaa 300
aagagcaaaa aactaaggtg tgcaaatcaa ctccaacgtt agagtaagtt atctattcag 360
ccttggaaaa catgtctttt ctagacaaga taagcataat caaagccttt tttagcttta 420
aactgttatc ctctaatttt tcaagaacag gagagtctgg gaataatcct aaagagtttt 480
ctatttgttg aagcagtcct agaattagtg agacactttt atggtagagt tctaagggag 540
aatttaagaa agttactttt tccttgttta ctcgtatttt taggtctaat tcggggaaat 600

<210> 49
<211> 600
<212> DNA
<213> Chlamydia

<400> 49
gatccgaatt cggcacgaga tgcttctatt acaattggtt tggatgcgga aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttggtg gaattgctga tactattgtt 120
gatagtacag tccaagatat tttagacaaa atcacaacag acccttctct aggtttgttg 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcactccc 240
aggaacattg aaactttatt aggaggaact gaaataggaa aattcacagt cacacccaaa 300
agctctggga gcatgttctt agtctcagca gatattattg catcaagaat ggaaggcggc 360

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gttgttctag ctttggtacg agaaggtgat tctaagccct acgcgattag ttatggatac 420
tcatcaggcg ttcctaattt atgtagtcta agaaccagaa ttattaatac aggattgact 480
ccgacaacgt attcattacg tgtaggcggt ttagaaagcg gtgtggtatg ggttaatgcc 540
ctttctaatg gcaatgatat tttaggaata acaaatactt ctaatgtatc ttttttggag 600

      <210> 50
      <211> 406
      <212> DNA
      <213> Chlamydia

      <400> 50
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gctatcaaat agcttattca gtctttcatt agttaaacga tcttttctag ccatgactca 120
tcctatgttc ttcagctata aaaatacttc ttaaaacttg atatgctgta atcaaatcat 180
cattaaccac aacataatca aattcgctag cggcagcaat ttcgacagcg ctatgctcta 240
atctttcttt cttctggaaa tctttctctg aatcccgagc attcaaacgg cgctcaagtt 300
cttcttgaga gggagcttga ataaaaatgt gactgccggc atttgcttct tcagagccaa 360
agctccttgt acatcaatca cggctatgca gtctcgtgcc gaattc                406

      <210> 51
      <211> 602
      <212> DNA
      <213> Chlamydia

      <400> 51
gatccgaatt cggcacgaga tattttagac aaaatcacaa cagacccttc tctaggtttg 60
ttgaaagctt ttaacaactt tccaatcact aataaaattc aatgcaacgg gttattcact 120
cccaggaaca ttgaaacttt attaggagga actgaaatag gaaaattcac agtcacaccc 180
aaaagctctg ggagcatgtt cttagtctca gcagatatta ttgcatcaag aatggaaggc 240
ggcgttgttc tagctttggt acgagaaggt gattctaagc cctacgcgat tagttatgga 300
tactcatcag gcgttcctaa tttatgtagt ctaagaacca gaattattaa tacaggattg 360
actccgacaa cgtattcatt acgtgtaggc ggtttagaaa gcggtgtggt atgggttaat 420
gccctttcta atggcaatga tattttagga ataacaaata cttctaatgt atcttttttg 480
gaggtaatac ctcaaacaaa cgcttaaaca atttttattg gatttttctt ataggtttta 540
tatttagaga aaaaagttcg aattacgggg tttgttatgc aaaataaact cgtgccgaat 600
tc                                                                602

      <210> 52
      <211> 145
      <212> DNA
      <213> Chlamydia

      <400> 52
gatccgaatt cggcacgagc tcgtgccgat gtgttcaaca gcatccatag gatgggcagt 60
caaatatact ccaagtaatt ctttttctct tttcaacaac tccttaggag agcgttggat 120
aacattttca gctcgtgccg aattc                                       145

      <210> 53
      <211> 450
      <212> DNA
      <213> Chlamydia

      <400> 53
gatccgaatt cggcacgagg taatcggcac cgcactgctg acactcatct cctcgagctc 60
gatcaaaccc acacttggga caagtaccta caacataacg gtccgctaaa aacttccctt 120
cttcctcaga atacagctgt tcggtcacct gattctctac cagtccgcgt tcctgcaagt 180
ttcgatagaa atcttgcaca atagcaggat gataagcgtt cgtagttctg gaaaagaaat 240
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attcttgata ccccatgcct gccaactctg cattaagggt aattgcgatt ccgtattcat 360
cagaaccaca aatatacaaa acctctttgc cttgtagtct ctgaaaacgc gcataaacat 420
ctgcaggcaa ataagcctcg tgccgaattc                                  450
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<210> 54
<211> 716
<212> DNA
<213> Chlamydia

<400> 54
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ccatccaaaa ggaaaaactg gtgaagcaag ctttaggaac acaatatcga gtagctgaaa 480
gctctccatc tccagaggga atcatagctc atcaagaagc ttctactcct tttcctggga 540
aaattacttt gatatatccc aataatatta cgcgctgtca gcgtttggcc gaggtatcca 600
aaaaatgatc gacaaggagc acgctaaatt tgtacatacc ccaaaatcaa tcagccatct 660
aggcaaatgg aatatcaaag taaacagtat acaactgggg atctcgtgcc gaattc 716

<210> 55
<211> 463
<212> DNA
<213> Chlamydia trachomatis

<400> 55
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cgcgttcggt taactatcaa tgggaatgtc gaagaatacg attacgttct cgtatctata 180
ggacgccgtt tgaatacaga aaatattggc ttggataaag ctggtgttat ttgtgatgaa 240
cgcggagtca tccctaccga tgccacaatg cgcacaaacg tacctaacat ttatgctatt 300
ggagatatca caggaaaatg gcaacttgcc catgtagctt ctcatcaagg aatcattgca 360
gcacggaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgatc 420
tttaccttcc ctgaagtcgc ttcagtaggc ctctccccaa cag 463

<210> 56
<211> 829
<212> DNA
<213> Chlamydia trachomatis

<400> 56
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tgaaagtaag aaagtcgtac agatcttgat ctgaaaagag aagaaggctt tttaattttc 660
tgcagagagc cagcgaggct tcaataatgt tgaagtctcc gacaccaggc aatgctaagg 720
cgacgatatt agttagtgaa gtctgagtat taaggaaatg aaggccaaag aaatagctat 780
caataaagaa gccttcttcc ttgactctaa agaatagtat gtcgtatcc 829

<210> 57
<211> 1537
<212> DNA
<213> Chlamydia trachomatis

<400> 57
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tgggtcagct gcttccgcag gaagtgcggc aggagcgttg aaatcctcta acaattcagg 180
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cccagccgaa atacaagcaa tcaaagatgc tcttgcgcaa gctttgaaac aaccatcagc 420
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ttttacagcc ggcatccggc ttctcgcgaa gtataac 1537

<210> 58
<211> 463
<212> DNA
<213> Chlamydia trachomatis

<400> 58
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cgcgttcggt taactatcaa tgggaatgtc gaagaatacg attacgttct cgtatctata 180
ggacgccgtt tgaatacaga aaatattggc ttggataaag ctggtgttat ttgtgatgaa 240
cgcggagtca tccctaccga tgccacaatg cgcacaaacg tacctaacat ttatgctatt 300
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gcacggaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgatc 420
tttaccttcc ctgaagtcgc ttcagtaggc ctctccccaa cag 463

<210> 59
<211> 552
<212> DNA
<213> Chlamydia trachomatis

<400> 59
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ttcataaaga ggaagacaaa caacgaaaag aagcttctga tgtgaaaaat gaagccgatg 240
gaatgatctt tagagccgaa aaagctgtga aagattacca cgacaaaatt cctgcagaac 300
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aagctatgca ggctcaatcc gcatccgcag cagcatcttc tgcagcgaat gctcaaggag 480
ggccaaacat taactccgaa gatctgaaaa aacatagttt cagcacacga cctccagcag 540
gaggaagcgc ct 552

<210> 60

<211> 1180
<212> DNA
<213> Chlamydia trachomatis

<400> 60
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acaacttttt catcttggat agagttagtt tttagaacta agtcttctgc ttacaatgct 180
cttgcatatt acgagctttt tataaacctc cccaaccaaa ctctacaaaa agagtttcaa 240
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<210> 61
<211> 1215
<212> DNA
<213> Chlamydia trachomatis

<400> 61
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aaatggggag attgttgcta cgcaaggaaa agctttgaac acaacagcca agcgggatgc 180
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tcccagatta ttgagaaaga actttcatgc gatgctacga ttggaccaga atcgtatgca 300
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tatcgcagag acgatagcgg atcgtgattg gttagagaat attatggtgc cttctgtaca 480
gagtcgtggt agtgcagtaa ttgaagcacg agggaagtct tcggcagctt ctgcagcacg 540
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ggtacagact tgagctctca aaagtttgct acagattctt acatcgcaga cccttattct 720
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catacaggct ttgaa 1215

<210> 62
<211> 688
<212> DNA
<213> Chlamydia trachomatis

<400> 62
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ctaacacttt atcagcgtca tctttgagaa gcatctcaat gagcgctttt tcttctctag 120
catgccgcac atccgcttct tcatgttctg tgaaatatgc atagtcttca ggattggaaa 180
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cttcatccat caagttatct aacaataact tacgcgcctc taaatcatcg caacgactat 480
gaatcgcaga taaatattta ggaaaggctt tgatatgtaa ataatagtct ttggcacgag 540
cctgtaattg ctctttagta agctcccct tcgaccattt cacataaaac gtgtgttcta 600
gcatatgctt attttgaata attaaatcta actgatctaa aaaattcata aacacctcca 660
tcatttcttt tcttgactcc acgtaacc 688

<210> 63
<211> 269
<212> DNA
<213> Chlamydia trachomatis

<400> 63
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tttggaaaat tgaccgctta ggacaaggcg aaaagagtaa aattactgta tgggtaaaac 240
ctcttaaaga aggttgctgc tttacagct 269

<210> 64
<211> 1339
<212> DNA
<213> Chlamydia trachomatis

<400> 64
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ccccggcgaa ggatcttggt attctctccg cctgggaagc tggtgagctg cgttacaaac 180
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cacatagaga gtttctcccg taattgcgct agctagggga gagactaaga aggctgctgc 300
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aaagagtttc cttgtcaaat tcttatatgg gtagagttaa tcaactgttt tcaagtgatt 1260
tatgtttatt ttaaaataat ttgttttaac aactgtttaa tagttttaat ttttaaagtg 1320
tgaaaaacag gttttatat 1339

<210> 65
<211> 195
<212> PRT
<213> Chlamydia trachomatis

<400> 65
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5 10 15

Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg Gly
20 25 30

Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val Cys
35 40 45

Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu Glu
50 55 60

His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr His
65 70 75 80

Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly Thr
85 90 95

Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe
100 105 110

Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu
115 120 125

Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro
130 135 140

Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu Ile
145 150 155 160

Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser Gly
165 170 175

Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe Gln
180 185 190

Thr Met Asp
195

<210> 66
<211> 520
<212> DNA
<213> Chlamydia

<400> 66
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tgatgtaaat tagcgcaatt agagggggat gaggttactt ggaaatataa ggagcgaagc 180
gatgaaggag atgtatttgc tctggaagca aaggtttctg aagctaacag aacattgcgt 240
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tcatcgaacg aatttttcaa tcctcgaaaa tcttctccag agacttcgga aagatcttct 480
gtgaaacgat cttcaagagg agtatcgcct ttttcctctg 520

<210> 67
<211> 276
<212> DNA
<213> Chlamydia

<400> 67

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caagggcact atcaggaccc aagagcttca gattatgacc tcccacgtgc tagcgactat 180
gatttgccta gaagcccata tcctactcca cctttgcctt ctagatatca gctacagaat 240
atggatgtag aagcagggtt ccgtgaggca gtttat                            276

      <210> 68
      <211> 248
      <212> DNA
      <213> Chlamydia

      <400> 68
gatccgaatt cggcacgagg tgttcaagaa tatgtccttc aagaatgggt taaattgaaa 60
gatctaccgg tagaagagtt gctagaaaaa cgatatcaga aattccgaac gataggtcta 120
tatgaaactt cttctgaaag cgattctgag gcataagaag catttagttt tattcggttt 180
ttctctttta tccatattag ggctaacgat aacgtctcaa gcagaaattt tttctctagg 240
tcttattg                                                           248

      <210> 69
      <211> 715
      <212> DNA
      <213> Chlamydia

      <220>
      <221> misc_feature
      <222> 34
      <223> n=A,T,C or G

      <400> 69
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attttcatat agttttcgac ggaactcttt attaaactcc caaaaccgaa tgttagtcgt 180
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tggtagagcc ggtatagcgc tctagcatgt cacaggcgat tgtttcttcg ctgatttttt 660
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      <210> 70
      <211> 323
      <212> DNA
      <213> Chlamydia

      <400> 70
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      <210> 71
      <211> 715
      <212> DNA
      <213> Chlamydia

      <400> 71
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acgtggatgt tttcgctgaa atctatcagg tccctgtttc tcgaggatcc atgttttcgg 240
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<210> 72
<211> 641
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 550,559,575,583,634,638
<223> n=A,T,C or G

<400> 72
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gaaaccttgn tctcttcgnc tctctcctgt agcanacaaa tgnctctctc gacatctctt 600
tcagcgtatt cggactgatg ccctaaagat cccnggangt t 641

<210> 73
<211> 584
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 460,523,541,546
<223> n=A,T,C or G

<400> 73
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gacttattac ggaacgagta aggcggagat ttctagagtt ctgcaaaagg gtaagcactg 180
catagccgtg attgatgtac aaggagcttt ggctctgaag aagcaaatgc cggcagtcac 240
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aagtattttt atagctgaag aacataggat gagtcatggn tagaaaagat cgtttaacta 480
atgaaagact gaataagcta tttgatagcc cctttagttt ggntaattac gtaattaagc 540
nagctnagaa caaaattgct agaggagatg ttcgttcttc taac 584

<210> 74
<211> 465
<212> DNA

<213> Chlamydia

<400> 74
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taagaaatta ttttcgagtg aaagagctag gcgtaatcat tacagatagc catactactc 120
caatgcggcg tggagtactg ggtatcgggc tgtgttggta tggattttct ccattacaca 180
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ttaccgtgga gtcaagaaaa gaaatgatgg aggtgtttat gaatt 465

<210> 75
<211> 545
<212> DNA
<213> Chlamydia

<400> 75
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aaagttttct tccaaaaacc tcttcctctc ttgattagtg atccctctgc aactacttta 120
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taagc 545

<210> 76
<211> 797
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 788,789
<223> n=A,T,C or G

<400> 76
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aaagttgnng gggaata 797

<210> 77
<211> 399
<212> DNA
<213> Chlamydia

<400> 77

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atcattaaaa agttgaagtt agatcctgag gcaagagcct ctgaattaac tgaagaagaa 180
gtaggacgac tgaactctct gctacaatca gaatataccg tagaagggga tttgcgacgt 240
cgtgttcaat cggatatcaa aagattgatc gccatccatt cttatcgagg tcagagacat 300
agactttctt taccagtaag aggacaacgt acaaaaacta attctcgtac tcgaaaaggt 360
aaaagaaaaa cagtcgcagg taagaagaaa taagaattc                        399
```

<210> 78
<211> 285
<212> DNA
<213> Chlamydia

<400> 78

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gtgaatattt ccacagattt agcagttata gttggcaagg gacctatgcc cagaaccgaa 120
attgtaaaga aagtttggga atacattaaa aaacacaact gtcaggatca aaaaaataaa 180
cgtaatatcc ttcccgatgc gaatcttgcc aaagtctttg gctctagtga tcctatcgac 240
atgttccaaa tgaccaaagc cctttccaaa catattgtaa aataa                 285
```

<210> 79
<211> 950
<212> DNA
<213> Chlamydia

<400> 79

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tgcgttataa ttctaagttt aaagaggaaa aatgaaagaa gagaaaaagt tgctgcttcg 900
cgaggttgaa gaaaagataa ccgcttctca aggttttatt ttgttgagat            950
```

<210> 80
<211> 395
<212> DNA
<213> Chlamydia

<400> 80

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agtaggtgtt cctacttgcg atagcatcgt tcctagtcct gatatccaca ggttgttata 180
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<210> 81
<211> 2085
<212> DNA
<213> Chlamydia

<400> 81
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<210> 82
<211> 405
<212> DNA
<213> Chlamydia

<400> 82
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gcaatcatta tgcaacgagt ggtttgaaaa gcgggtacaa tattgggagt accgatgggt 120
ttctccctgt cattgggcct gttatatggg agtcggaggg tcttttccgc gcttatattt 180
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gcaaaaaata aattagctcc tccattccga actgcagaat ttgat 405

<210> 83
<211> 379
<212> DNA
<213> Chlamydia

<400> 83
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ttccctacgt atcactttgc taatgtagtt gatgatcatt tgatggggat tacccatgtg 180

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ctttccaaga gaaagaatcc tacttctatt ttttactatc gggatgctgg atacaaaaaa 360
gaagcgttca tgaatttcc                                              379
```

<210> 84
<211> 715
<212> DNA
<213> Chlamydia

<400> 84

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caaagacgca gttttgagtg ttatacaaat aaaaaccaga atttcccatt ttaaaactct 660
tttttatttt gagctttaaa taaattaggt ttttagtttc aagtttgcta ttaat       715
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<210> 85
<211> 476
<212> DNA
<213> Chlamydia

<400> 85

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<210> 86
<211> 1551
<212> DNA
<213> Chlamydia

<400> 86

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<210> 87
<211> 3031
<212> DNA
<213> Chlamydia

<400> 87
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<210> 88
<211> 976
<212> DNA
<213> Chlamydia

<400> 88

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<210> 89
<211> 94
<212> PRT
<213> Chlamydia

<400> 89

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Met His His His His His His Met Ser Gln Lys Asn Lys Asn Ser Ala
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Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly
            20                  25                  30

Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr
        35                  40                  45

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu
    50                  55                  60

Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp
65                  70                  75                  80

Met Phe Gln Met Thr Lys Ala Leu Ser Lys His Ile Val Lys
                85                  90
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<210> 90
<211> 474
<212> PRT
<213> Chlamydia

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<400> 90
Met Ala Ser His His His His His His Met Asn Glu Ala Phe Asp Cys
                  5                  10                  15

Val Val Ile Gly Ala Gly Pro Gly Gly Tyr Val Ala Ala Ile Thr Ala
             20                  25                  30

Ala Gln Ala Gly Leu Lys Thr Ala Leu Ile Glu Lys Arg Glu Ala Gly
         35                  40                  45

Gly Thr Cys Leu Asn Arg Gly Cys Ile Pro Ser Lys Ala Leu Leu Ala
     50                  55                  60

Gly Ala Glu Val Val Thr Gln Ile Arg His Ala Asp Gln Phe Gly Ile
 65                  70                  75                  80

His Val Glu Gly Phe Ser Ile Asn Tyr Pro Ala Met Val Gln Arg Lys
                 85                  90                  95

Asp Ser Val Val Arg Ser Ile Arg Asp Gly Leu Asn Gly Leu Ile Arg
            100                 105                 110

Ser Asn Lys Ile Thr Val Phe Ser Gly Arg Gly Ser Leu Ile Ser Ser
        115                 120                 125

Thr Glu Val Lys Ile Leu Gly Glu Asn Pro Ser Val Ile Lys Ala His
    130                 135                 140

Ser Ile Ile Leu Ala Thr Gly Ser Glu Pro Arg Ala Phe Pro Gly Ile
145                 150                 155                 160

Pro Phe Ser Ala Glu Ser Pro Arg Ile Leu Cys Ser Thr Gly Val Leu
                165                 170                 175

Asn Leu Lys Glu Ile Pro Gln Lys Met Ala Ile Ile Gly Gly Gly Val
            180                 185                 190

Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val
        195                 200                 205

Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Asn Pro Asp
    210                 215                 220

Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe
225                 230                 235                 240

Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val
                245                 250                 255

Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val
            260                 265                 270

Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala
        275                 280                 285

Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met
    290                 295                 300

Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys
305                 310                 315                 320
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Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg
325 330 335

Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser
340 345 350

Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr
355 360 365

Ala Ala Gln Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe
370 375 380

Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala
385 390 395 400

Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val
405 410 415

Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val
420 425 430

Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His
435 440 445

Pro Thr Leu Ala Glu Val Trp Ala Glu Ser Ala Leu Leu Ala Val Asp
450 455 460

Thr Pro Leu His Met Pro Pro Ala Lys Lys
465 470

<210> 91
<211> 129
<212> PRT
<213> Chlamydia

<400> 91
Met His His His His His His Met Pro Arg Ile Ile Gly Ile Asp Ile
5 10 15

Pro Ala Lys Lys Lys Leu Lys Ile Ser Leu Thr Tyr Ile Tyr Gly Ile
20 25 30

Gly Ser Ala Arg Ser Asp Glu Ile Ile Lys Lys Leu Lys Leu Asp Pro
35 40 45

Glu Ala Arg Ala Ser Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn
50 55 60

Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg Arg Arg
65 70 75 80

Val Gln Ser Asp Ile Lys Arg Leu Ile Ala Ile His Ser Tyr Arg Gly
85 90 95

Gln Arg His Arg Leu Ser Leu Pro Val Arg Gly Gln Arg Thr Lys Thr
100 105 110

Asn Ser Arg Thr Arg Lys Gly Lys Arg Lys Thr Val Ala Gly Lys Lys
115 120 125

Lys

<210> 92
<211> 202
<212> PRT
<213> Chlamydia

<400> 92
Met His His His His His His Met Gly Ser Leu Val Gly Arg Gln Ala
5 10 15

Pro Asp Phe Ser Gly Lys Ala Val Val Cys Gly Glu Glu Lys Glu Ile
20 25 30

Ser Leu Ala Asp Phe Arg Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro
35 40 45

Lys Asp Phe Thr Tyr Val Cys Pro Thr Glu Leu His Ala Phe Gln Asp
50 55 60

Arg Leu Val Asp Phe Glu Glu His Gly Ala Val Val Leu Gly Cys Ser
65 70 75 80

Val Asp Asp Ile Glu Thr His Ser Arg Trp Leu Thr Val Ala Arg Asp
85 90 95

Ala Gly Gly Ile Glu Gly Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser
100 105 110

Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu
115 120 125

Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His
130 135 140

Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu
145 150 155 160

Arg Ile Leu Asp Ser Leu Ile Phe Phe Glu Asn His Gly Met Val Cys
165 170 175

Pro Ala Asn Trp Arg Ser Gly Glu Arg Gly Met Val Pro Ser Glu Glu
180 185 190

Gly Leu Lys Glu Tyr Phe Gln Thr Met Asp
195 200

<210> 93
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> made in a lab

<400> 93

Glu Asn Ser Leu Gln Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp
1 5 10 15
Asp Lys Leu

<210> 94
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 94
Asp Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys
1 5 10 15
Val Phe Gly Thr
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<210> 95
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 95
Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr
1 5 10 15
Glu Lys Pro Ile
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<210> 96
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 96
Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met
1 5 10 15
Phe Gln Met Thr
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<210> 97
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 97
Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr Lys
1 5 10 15
Met Val Ser Gln
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<210> 98
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 98
Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly
1 5 10 15
Thr Glu Lys Pro
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<210> 99
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 99
Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly
1 5 10 15

<210> 100
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 100
Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp Pro Thr
1 5 10 15

<210> 101
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 101
Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys
1 5 10 15
Gln Asp Gln Lys
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<210> 102
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 102

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 1               5                  10                  15
Lys Arg Asn Ile
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<210> 103
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 103
Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys
 1               5                  10                  15

<210> 104
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 104
Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
 1               5                  10                  15
Ser Asp Tyr Val
            20

<210> 105
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 105
Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg Arg Arg Val Gln
 1               5                  10                  15
Ser Asp Ile Lys Arg
            20

<210> 106
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 106
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys
 1               5                  10                  15
Ile Ser Leu Thr
            20

<210> 107
<211> 20
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<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 107
Ala Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln
1 5 10 15
Ser Asp Tyr Val
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<210> 108
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 108
Leu Asn Ala Leu Leu Gln Ser Asp Tyr Val Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
20

<210> 109
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 109
Leu Asn Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg
1 5 10 15
Arg Arg Val Gln
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<210> 110
<211> 1461
<212> DNA
<213> Chlamydia

<400> 110
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tgcctagaag cccatatcct actccacctt tgccttctag atatcagcta cagaatatgg 180
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ctacacaaga tggttggata g 1461

<210> 111
<211> 267
<212> DNA
<213> Chlamydia

<400> 111
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acagaattcg tggaggattc cgggtttgcg cagttaaagc tccaggcttt ggagatagaa 120
gaaaagctat gttggaagac atcgctatct taactggcgg tcaactcatt agcgaagagt 180
tgggcatgaa attagaaaac gctaacttag ctatgttagg taaagctaaa aaagttatcg 240
tttctaaaga agacacgacc atcgtcg 267

<210> 112
<211> 698
<212> DNA
<213> Chlamydia

<400> 112
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agatctgagc caactgaaaa aatacacagt tctctacatc aagaagctgc tcgaaaccta 180
cagacaactc gggcatcgaa agacaaaaat tgcaaaattt gatgacctac ctaccgagag 240
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cgataatttt accgatatct cccttagcaa cagtcaattc gtagataatc gtattggttc 600
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ctaaaaactc tttcatgcga agcaaatcct acacaagc 698

<210> 113
<211> 1142
<212> DNA
<213> Chlamydia

<400> 113
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aacgaaaaaa gaaggtattt tgattccttc tgcagggatt gatgaatcga atacggacca 180
gccttttgtt ttatatccta aagatatttt gggatcgtgt aatcgcatcg gagaatggtt 240
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ttaattattc aaaataagca tatgctagaa cacacgtttt atgtgaaatg gtcgaagggg 720
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cagtttgtgt ttgctctagg agttactcca gaagagttag aggctcatga gcctagtgaa 960
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ca 1142

<210> 114
<211> 976
<212> DNA
<213> Chlamydia

<400> 114
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ggcacaaagt accttctggg cgcactactt taaagattcg tcgtcctttt ggtactacga 180
gagaagttcg tgtgaaatgg cgttatgttc ctgaaggtgt aggagatttg gctaccatag 240
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cagagcttcg caatcattat gcaacgagtg gtttgaaaag cgggtacaat attgggagta 420
ccgatgggtt tctccctgtc attgggcctg ttatatggga gtcggagggt ctttttccgcg 480
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aaacgaacaa cccaggtggt agtgtccttt atctttatgc actgctttcc atgttgacag 720
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ttggacgtca agtattgaat tgttggagta aaggggatat cgagttatca acacctattc 960
ctctttttgg ttttga 976

<210> 115
<211> 995
<212> DNA
<213> Chlamydia

<400> 115
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cgccgtcttc gacttaggag gaggaacttt cgatatttct atcttggaaa tcggtgacgg 660
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agtcatcatc aactggatgc ttgatgaatt caaaaaacaa gaaggcattg atctaagcaa 780
agataacatg gctttgcaaa gattgaaaga tgctgctgaa aaagcaaaaa tagaattgtc 840
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gcgaaccaaa caaccttgtg ctcaggcttt aaaag 995

<210> 116
<211> 437
<212> DNA
<213> Chlamydia

<400> 116
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catggtggtg gagcctttgt taccaaagaa atctctcaga cttacacctc tgatgtggaa 420
acaattccag gaatcac 437

<210> 117
<211> 446
<212> DNA
<213> Chlamydia

<400> 117
aagtttacct agaccaaact gaagatgacg aaggaaaagt tgttttatcc agagaaaaag 60
caacaagaca acgacaatgg gaatacattc ttgctcactg cgaggaaggt tctattgtta 120
agggacaaat tacccgaaaa gttaagggtg gtttgatcgt agatattggt atggaagcct 180
tccttccagg atcccaaata gacaataaga agatcaagaa cttagatgat tacgtaggca 240
aggtttgtga gttcaaaatt ctcaaaatca acgtggatcg tcggaacgtt gttgtatcta 300
gaagagaact tctcgaagct gaacgcattt ctaagaaagc agagttgatc gagcaaatca 360
ctatcggtga acgtcgcaaa ggtatcgtta agaatatcac agatttcgga gtattcttgg 420
atcttgatgg cattgacggc ctactc 446

<210> 118
<211> 951
<212> DNA
<213> Chlamydia

<400> 118
agtattgcga aatattactg tgagaagcaa tgctgagagc ggttctagta aaagtgaggg 60
gagagctgtc agaagggatc gctcaggaag cgagacaacg tgtggctgat ttattaggaa 120
gattccctct ttatcctgaa atcgatctgg aaacgctagt ttagtgggag actctatgcc 180
tgaaggggaa atgatgcata agttgcaaga tgtcatagat agaaagttgt tggattctcg 240
tcgtattttc ttctccgaac ctgtaacgga gaaaagtgct gcagaagcca tcaaaaagct 300
ttggtatttg gaactcacca atcctgggca gccaattgta tttgtcatta atagccctgg 360
agggtctgtt gatgctgggt ttgctgtttg ggaccaaatt aaaatgatct cttctccttt 420
gactacagtt gttacaggtt tagcagcatc tatgggatct gtattgagtt tgtgtgctgt 480
tccaggaaga cgttttgcta cgcctcatgc gcgcattatg attcaccagc cttctattgg 540
aggaaccatt actggtcaag ccacggactt ggatattcat gctcgtgaaa ttttaaaaac 600
aaaagcacgc attattgatg tgtatgtcga ggcaactgga caatctccag aggtgataga 660
gaaagctatc gatcgagata tgtggatgag tgcaaatgaa gcaatggagt ttggactgtt 720
agatgggatt ctcttctctt ttacgactt gtagatatct tttatattct ggagcaggaa 780
acagtttcat tttgggagaa tcgatgcctt ctcttgagga tgttctgttt ttatgccagg 840
aagagatggt tgatgggttt ttatgtgtag agtcttctga aatagcagat gctaaactca 900
ctgtttttaa tagtgatgga tctatcgcgt ctatgtgcgg gaatgggttg c 951

<210> 119
<211> 953
<212> DNA
<213> Chlamydia

<400> 119
atatcaaagt tgggcaaatg acagagccgc tcaaggacca gcaaataatc cttgggacaa 60
catcaacacc tgtcgcagcc aaaatgacag cttctgatgg aatatcttta acagtctcca 120
ataatccatc aaccaatgct tctattacaa ttggtttgga tgcggaaaaa gcttaccagc 180
ttattctaga aaagttggga gatcaaattc ttggtggaat tgctgatact attgttgata 240
gtacagtcca agatatttta gacaaaatca caacagaccc ttctctaggt ttgttgaaag 300
cttttaacaa ctttccaatc actaataaaa ttcaatgcaa cgggttattc actcccagga 360
acattgaaac tttattagga ggaactgaaa taggaaaatt cacagtcaca cccaaaagct 420

```
ctgggagcat gttcttagtc tcagcagata ttattgcatc aagaatggaa ggcggcgttg 480
ttctagcttt ggtacgagaa ggtgattcta agccctacgc gattagttat ggatactcat 540
caggcgttcc taatttatgt agtctaagaa ccagaattat taatacagga ttgactccga 600
caacgtattc attacgtgta ggcggtttag aaagcggtgt ggtatgggtt aatgcccttt 660
ctaatggcaa tgatatttta ggaataacaa atacttctaa tgtatctttt ttggaggtaa 720
tacctcaaac aaacgcttaa acaattttta ttggattttt cttataggtt ttatatttag 780
agaaaaaagt tcgaattacg ggtttgtta tgcaaaataa aagcaaagtg agggacgatt 840
ttattaaaat tgttaaagat tcctggtatc ggtctgcgat tccgactcgt ccaacatcaa 900
tacaacctat taatttcccc tcgtcaaaaa taaggttatc aagtgagaaa tca        953
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<210> 120
<211> 897
<212> DNA
<213> Chlamydia

<220>
<221> misc_feature
<222> 395
<223> n = A,T,C or G

<400> 120

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atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg 360
ctcgtagcag atctttgtgt gtctcataag cgcanagcgg ctgcggctgt ctgtagcttc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg cgcaaccgtt tctttcttcc caaattaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt 600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc 660
gaattgtcgg gagaggaaaa tgcttgcgag aggagagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg 840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcgccag agcataa    897
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<210> 121
<211> 298
<212> PRT
<213> Chlamydia

<400> 121

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1              5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
```

```
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Ala Arg Ala
    290                 295
```

<210> 122
<211> 897
<212> DNA
<213> Chlamydia

<400> 122

```
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtggcttc     420
atcggaggaa ttacctacct cgcgacattc ggagttatcc gtccgattct gtttgtcaac     480
aaaatgctgg tgaacccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgtcgg gagaggaaaa tgcttgcgag aagagagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
```

<210> 123
<211> 298
<212> PRT
<213> Chlamydia

<400> 123

```
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
```

```
                85                      90                      95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                     105                     110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                     120                     125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
    130                     135                     140
Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
145                     150                     155                     160
Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                     170                     175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                     185                     190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                     200                     205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
    210                     215                     220
Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
225                     230                     235                     240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                     250                     255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                     265                     270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                     280                     285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                     295
```

<210> 124
<211> 897
<212> DNA
<213> Chlamydia

<400> 124

```
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 125
<211> 298
<212> PRT
<213> Chlamydia

<400> 125

```
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
```

```
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295
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<210> 126
<211> 897
<212> DNA
<213> Chlamydia

<400> 126

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atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaagtgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 127
<211> 298
<212> PRT
<213> Chlamydia

<400> 127
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

<210> 128
<211> 897
<212> DNA
<213> Chlamydia

<400> 128
atggcttcta tatgtggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga 240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg 360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtggcttc 420
atcggaggaa ttacctacct cgcgacattc ggagttatcc gtccgattct gtttgtcaac 480
aaaatgctgg tgaacccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt 600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc 660
gaagtgtcgg gagaggaaaa tgcttgcgag aagagagtcg ctggagagaa agccaagacg 720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc 780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct 840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa 897

<210> 129
<211> 298
<212> PRT
<213> Chlamydia

<400> 129
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1 5 10 15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
20 25 30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
35 40 45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
50 55 60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Thr Arg
65 70 75 80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
85 90 95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
100 105 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
115 120 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Gly Phe Ile Gly Gly Ile
130 135 140
Thr Tyr Leu Ala Thr Phe Gly Val Ile Arg Pro Ile Leu Phe Val Asn
145 150 155 160
Lys Met Leu Val Asn Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
165 170 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
180 185 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
195 200 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Ser Gly
210 215 220
Glu Glu Asn Ala Cys Glu Lys Arg Val Ala Gly Glu Lys Ala Lys Thr
225 230 235 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
245 250 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
260 265 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
275 280 285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
290 295

<210> 130
<211> 897
<212> DNA
<213> Chlamydia

<400> 130
atggctgcta tatgtggacg tttagggtct ggtacaggga atgctctaaa agcttttttt 60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact 120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc 180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga 240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg 300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg 360
ctcgtagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc 420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac 480
aaaatgctgg cgcaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt 540

```
agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt      600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc      660
gaattgtcgg gagaggaaaa tgcttgcgag aggggagtcg ctggagagaa agccaagacg      720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc      780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg      840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcaacag agtataa         897
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<210> 131
<211> 298
<212> PRT
<213> Chlamydia

<400> 131

```
Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1               5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Gly Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
    290                 295
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<210> 132
<211> 897
<212> DNA
<213> Chlamydia

<400> 132

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atggctgcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt       60
acacagccca gcaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact      120
gttaaggtcg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc      180
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gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttctcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctcttacat gaaagctgct agtcagaaac cgcaagaagg ggatgagggg     360
ctcgtagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcttc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg cgcaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tttgtggtgg gttctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgtcactc     660
gaattgtcgg gagaggaaaa tgcttgtgag aggagagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gttgcctatt acaatgggta ttcgtgcaat tgtggctgcg     840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcaacag agtataa        897
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<210> 133
<211> 298
<212> PRT
<213> Chlamydia

<400> 133

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Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
1               5                   10                  15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val
            180                 185                 190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val
        275                 280                 285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val
    290                 295
```

<210> 134
<211> 897
<212> DNA

<213> Chlamydia

<400> 134

```
atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agcttttttt      60
acacagccca acaataaaat ggcaagggta gtaaataaga cgaagggaat ggataagact     120
attaaggttg ccaagtctgc tgccgaattg accgcaaata ttttggaaca agctggaggc     180
gcgggctctt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatgcgaga     240
actgttgtcg ctttagggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg     300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg ggatgagggg     360
ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc     420
atcggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac     480
aaaatgctgg caaaaccgtt tctttcttcc caaactaaag caaatatggg atcttctgtt     540
agctatatta tggcggctaa ccatgcagcg tctgtggtgg gtgctggact cgctatcagt     600
gcggaaagag cagattgcga agcccgctgc gctcgtattg cgagagaaga gtcgttactc     660
gaaatgccgg gagaggaaaa tgcttgcgag aagaaagtcg ctggagagaa agccaagacg     720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttgga atgcgttgcc     780
gacgttttca aattggtgcc gctgcctatt acaatgggta ttcgtgcgat tgtggctgct     840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa        897
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<210> 135
<211> 298
<212> PRT
<213> Chlamydia

<400> 135

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Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu
 1               5                  10                  15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn
            20                  25                  30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser
    50                  55                  60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr
                85                  90                  95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln
            100                 105                 110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser
        115                 120                 125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile
    130                 135                 140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn
145                 150                 155                 160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met
                165                 170                 175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val
            180                 185                 190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala
        195                 200                 205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Met Pro Gly
    210                 215                 220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr
225                 230                 235                 240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu
                245                 250                 255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met
            260                 265                 270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile
        275                 280                 285
```

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Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala
    290                 295

      <210> 136
      <211> 882
      <212> DNA
      <213> Chlamydia

      <400> 136
atggcttctg tatgtgggcg attaagtgct ggggtgggga acagatttaa cgcatttttc      60
acgcgtcccg gtaacaagct atcacggttt gtaaatagcg caaaaggatt agacagatca     120
ataaaggttg ggaagtctgc tgctgaatta acggcgagta ttttagagca aactgggggg     180
gcagggactg atgcacatgt tacggcggcc aaggtgtcta aagcacttgg ggacgcgcga     240
acagtaatgg ctctagggaa tgtcttcaat gggtctgtgc cagcaaccat tcaaagtgcg     300
cgaagctgtc tcgcccattt acgagcggcc ggcaaagaag aagaaacatg ctccaaggtg     360
aaagatctct gtgtttctca tagacgaaga gctgcggctg aggcttgtaa tgttattgga     420
ggagcaactt atattacaac tttcggagcg attcgtccga cattactcgt taacaagctt     480
cttgccaaac cattcctttc ctcccaagcc aaagaagggt tgggagcttc tgttggttat     540
atcatggcag cgaaccatgc ggcatctgtg cttgggtctg ctttaagtat tagcgcagaa     600
agagcagact gtgaagagcg gtgtgatcgc attcgatgta gtgaggatgg tgaaatttgc     660
gaaggcaata aattaacagc tatttcggaa gagaaggcta gatcatggac tctcattaag     720
tacagattcc ttactatgat agaaaaacta tttgagatgg tggcggatat cttcaagtta     780
attcctttgc caatttcgca tggaattcgt gctattgttg ctgcgggatg tacgttgact     840
tctgcagtta ttggcttagg tactttttgg tctagagcat aa                        882

      <210> 137
      <211> 293
      <212> PRT
      <213> Chlamydia

      <400> 137
Met Ala Ser Val Cys Gly Arg Leu Ser Ala Gly Val Gly Asn Arg Phe
 1               5                  10                  15
Asn Ala Phe Phe Thr Arg Pro Gly Asn Lys Leu Ser Arg Phe Val Asn
            20                  25                  30
Ser Ala Lys Gly Leu Asp Arg Ser Ile Lys Val Gly Lys Ser Ala Ala
        35                  40                  45
Glu Leu Thr Ala Ser Ile Leu Glu Gln Thr Gly Gly Ala Gly Thr Asp
    50                  55                  60
Ala His Val Thr Ala Ala Lys Val Ser Lys Ala Leu Gly Asp Ala Arg
65                  70                  75                  80
Thr Val Met Ala Leu Gly Asn Val Phe Asn Gly Ser Val Pro Ala Thr
                85                  90                  95
Ile Gln Ser Ala Arg Ser Cys Leu Ala His Leu Arg Ala Ala Gly Lys
            100                 105                 110
Glu Glu Glu Thr Cys Ser Lys Val Lys Asp Leu Cys Val Ser His Arg
        115                 120                 125
Arg Arg Ala Ala Ala Glu Ala Cys Asn Val Ile Gly Gly Ala Thr Tyr
    130                 135                 140
Ile Thr Thr Phe Gly Ala Ile Arg Pro Thr Leu Leu Val Asn Lys Leu
145                 150                 155                 160
Leu Ala Lys Pro Phe Leu Ser Ser Gln Ala Lys Glu Gly Leu Gly Ala
                165                 170                 175
Ser Val Gly Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val Leu Gly
            180                 185                 190
Ser Ala Leu Ser Ile Ser Ala Glu Arg Ala Asp Cys Glu Glu Arg Cys
        195                 200                 205
Asp Arg Ile Arg Cys Ser Glu Asp Gly Glu Ile Cys Glu Gly Asn Lys
    210                 215                 220
Leu Thr Ala Ile Ser Glu Glu Lys Ala Arg Ser Trp Thr Leu Ile Lys
225                 230                 235                 240
```

```
Tyr Arg Phe Leu Thr Met Ile Glu Lys Leu Phe Glu Met Val Ala Asp
                245                 250                 255
Ile Phe Lys Leu Ile Pro Leu Pro Ile Ser His Gly Ile Arg Ala Ile
            260                 265                 270
Val Ala Ala Gly Cys Thr Leu Thr Ser Ala Val Ile Gly Leu Gly Thr
        275                 280                 285
Phe Trp Ser Arg Ala
    290

      <210> 138
      <211> 16
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 138
Asp Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser
 1               5                  10                  15

      <210> 139
      <211> 16
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 139
Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
 1               5                  10                  15

      <210> 140
      <211> 18
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 140
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile
 1               5                  10                  15
Arg Pro


      <210> 141
      <211> 18
      <212> PRT
      <213> Artificial Sequence

      <220>
      <223> Made in a lab

      <400> 141
Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn Lys
 1               5                  10                  15
Met Leu
```

<210> 142
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 142
Arg Pro Ile Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser
1 5 10 15
Ser Gln

<210> 143
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 143
Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met Gly
1 5 10 15
Ser

<210> 144
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 144
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 145
Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 146
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 146

Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 147
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 147
Cys Ser Phe Ile Gly Gly Ile Thr Tyr
1 5

<210> 148
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 148
Cys Ser Phe Ile Gly Gly Ile Thr
1 5

<210> 149
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 149
Cys Ser Ile Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 150
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 150
Cys Gly Phe Ile Gly Gly Ile Thr Tyr Leu
1 5 10

<210> 151
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 151
Gly Phe Ile Gly Gly Ile Thr Tyr Leu

1 5

<210> 152
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 152
Gln Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Arg Leu
1 5 10 15
Ser Val Ala Ser
20

<210> 153
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 153
Glu Arg Leu Arg Leu Arg Leu Ser Val Ala Ser Ser Glu Glu Leu Pro
1 5 10 15
Thr Ser Arg His
20

<210> 154
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 154
Ala Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val
1 5 10 15
Arg Phe Cys Leu
20

<210> 155
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 155
Arg His Ser Glu Leu Ser Val Arg Phe Cys Leu Ser Thr Lys Cys Trp
1 5 10 15
Arg Asn Arg Phe
20

<210> 156
<211> 20
<212> PRT

<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 156
Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys Leu Lys
1 5 10 15
Gln Ile Trp Asp
20

<210> 157
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 157
Ile Phe Val Cys Leu Ile Ser Ala Glu Arg Leu Arg Leu Ser Val Ala
1 5 10 15
Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val Arg
20 25 30
Phe Cys Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys
35 40 45
Leu Lys Gln Ile Trp
50

<210> 158
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 158
Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe
1 5 10 15
Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile
20 25 30
Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile
35 40 45
Lys Ala Asn Met
50

<210> 159
<211> 24
<212> DNA
<213> Chlamydia

<400> 159
ttttgaagca ggtaggtgaa tatg 24

<210> 160
<211> 24
<212> DNA
<213> Chlamydia

<400> 160

ttaagaaatt taaaaaatcc ctta 24

<210> 161
<211> 24
<212> DNA
<213> Chlamydia

<400> 161
ggtataatat ctctctaaat tttg 24

<210> 162
<211> 19
<212> DNA
<213> Chlamydia

<400> 162
agataaaaaa ggctgtttc 19

<210> 163
<211> 24
<212> DNA
<213> Chlamydia

<400> 163
ttttgaagca ggtaggtgaa tatg 24

<210> 164
<211> 29
<212> DNA
<213> Chlamydia

<400> 164
tttacaataa gaaaagctaa gcactttgt 29

<210> 165
<211> 20
<212> DNA
<213> Chlamydia

<400> 165
ccttacacag tcctgctgac 20

<210> 166
<211> 20
<212> DNA
<213> Chlamydia

<400> 166
gtttccgggc cctcacattg 20

<210> 167
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 167
Ser Phe Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 168
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 168
Ser Ile Ile Gly Gly Ile Thr Tyr Leu
1 5

<210> 169
<211> 2643
<212> DNA
<213> Chlamydia

<400> 169
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aatcatgtcg tctgtacatt ttttgaggac tgtaccatgg agagcctctt tcctgctctt 180
tgtgctcatg catcacaaga cgatcctttg tatgtacttg gaaattccta ctgttggttc 240
gtatctaaac tccatatcac ggaccccaaa gaggctcttt ttaaagaaaa aggagatctt 300
tccattcaaa actttcgctt cctttccttc acagattgct cttccaagga aagctctcct 360
tctattattc atcaaaagaa tggtcagtta tccttgcgca ataatggtag catgagtttc 420
tgtcgaaatc atgctgaagg ctctggagga gccatctctg cggatgcctt ttctctacag 480
cacaactatc ttttcacagc ttttgaagag aattcttcta aaggaaatgg cggagccatt 540
caggctcaaa ccttctcttt atctagaaat gtgtcgccta tttctttcgc ccgtaatcgt 600
gcggatttaa atggcggcgc tatttgctgt agtaatctta tttgttcagg gaatgtaaac 660
cctctctttt tcactggaaa ctccgccacg aatggaggcg ctatttgttg tatcagcgat 720
ctaaacacct cagaaaaagg ctctctctct cttgcttgta accaagaaac gctatttgca 780
agcaattctg ctaaagaaaa aggcggggct atttatgcca agcacatggt attgcgttat 840
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agcgaacgtc tttctgaaga agaaaaaact cctgataacc tcacttccca actacagcag 1260
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tcctctgatt tgaagttagc tacgctaagt attccccttc attccttaga tactgaaaaa 1440
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gatgagaatt tttatgaaaa tgtagagctt ctcagtaaag agcaaaacaa tattcctctc 1560
cttactctcc ctaaagagca atctcattta catcttcctg atgggaacct ctcttctcac 1620
tttggatatc aaggagattg gacttttct tggaaagatt ctgatgaagg gcattctctg 1680
attgctaatt ggacgcctaa aaactatgtg cctcatccag aacgtcaatc tacactcgtt 1740
gcgaacactc tttggaacac ctattccgat atgcaagctg tgcagtcgat gattaataca 1800
acagcgcacg gaggagccta tctatttgga acgtggggat ctgctgtttc taatttattc 1860
tatgttcacg acagctctgg gaaacctatc gataattggc atcatagaag ccttggctac 1920
ctattcggta tcagtactca cagtttagat gaccattctt tctgcttggc tgcaggacaa 1980
ttactcggga aatcgtccga ttcctttatt acgtctacag aaacgacctc ctatatagct 2040
actgtacaag cgcaactcgc tacctctcta atgaaaatct ctgcacaggc atgctacaat 2100
gaaagtatcc atgagctaaa aacaaaatat cgctccttct ctaaagaagg attcggatcc 2160
tggcatagcg ttgcagtatc cggagaagtg tgcgcatcga ttcctattgt atccaatggt 2220
tccggactgt tcagctcctt ctctattttc tctaaactgc aaggattttc aggaacacag 2280
gacggttttg aggagagttc gggagagatt cggtcctttt ctgccagctc tttcagaaat 2340
atttcacttc ctataggaat aacatttgaa aaaaaatccc aaaaaacacg aacctactat 2400
tactttctag gagcctacat ccaagacctg aaacgtgatg tggaatcggg acctgtagtg 2460
ttactcaaaa atgccgtctc ctgggatgct cctatggcga acttggattc acgagcctac 2520

atgttccggc ttacgaatca aagagctcta cacagacttc agacgctgtt aaatgtgtct 2580
tgtgtgctgc gtgggcaaag ccatagttac tccctggatc tggggaccac ttacaggttc 2640
tag 2643

<210> 170
<211> 2949
<212> DNA
<213> Chlamydia

<400> 170
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ataggagatc cgagtgggac tactgttttt tctgcaggag agttaacatt aaaaaatctt 120
gacaattcta ttgcagcttt gcctttaagt tgttttggga acttattagg gagttttact 180
gttttaggga gaggacactc gttgactttc gagaacatac ggacttctac aaatggggca 240
gctctaagta atagcgctgc tgatggactg tttactattg agggttttaa agaattatcc 300
ttttccaatt gcaattcatt acttgccgta ctgcctgctg caacgactaa taagggtagc 360
cagactccga cgacaacatc tacaccgtct aatggtacta tttattctaa aacagatctt 420
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gaaggcggag aaattatttg tggagtaccg acaagaaact cagctcgcgg agaatacagc    5220
acgcagctgt acccgggacc tttgtggact ctgtatggat cctacacgat agaagcagac    5280
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<210> 174
<211> 5265
<212> DNA
<213> Chlamydia

<400> 174

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accactttta ctgaaacaat tggagaagct ggggcagaat atatcgtctc tggtaacgca     180
tctttcacaa aatttaccaa cattcctact accgatacaa caactcccac gaactcaaac     240
tcctctagct ctagcggaga aactgcttcc gtttctgagg atagtgactc tacaacaacg     300
actcctgatc ctaaaggtgg cggcgccttt tataacgcgc actccggagt tttgtccttt     360
atgacacgat caggaacaga aggttcctta actctgtctg agataaaaat gactggtgaa     420
ggcggtgcta tcttctctca aggagagctg ctatttacag atctgacaag tctaaccatc     480
caaaataact tatcccagct atccggagga gcgatttttg gaggatctac aatctcccta     540
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ggaaatgatt cggtgtcttc ccccagttcc agtagagctg aacccgcagc agctaatctt     720
caaagtcact ttatttgtgc tacagctact cctgctgctc aaaccgatac agaaacatca     780
actccctctc ataagccagg atctggggga gctatctatg ctaaaggcga ccttactatc     840
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acaggaacta ttgtgttctc ttctgaatta catgaaaaca aatcttacat cccacagaat    3660
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aacatagcta acggagctct agctatcaat gggttaacga ttgatctttc cagtatgggg    3840
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ctatatcttg gtcccttctg gactctctac ggaaactata ctatcgatgt aggcatgtat    5220
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<210> 175
<211> 880
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 336
<223> Xaa = Any Amino Acid

<400> 175
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Ile Leu Ser Ser Thr Ala Val Leu Phe Gly Gln Asp Pro Leu Gly Glu
            20                  25                  30
Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr Phe Phe
        35                  40                  45
Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala His Ala
    50                  55                  60
Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys Trp Phe
65                  70                  75                  80
Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe Lys Glu
                85                  90                  95
Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe Thr Asp
            100                 105                 110
Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys Asn Gly
        115                 120                 125
Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg Asn His
    130                 135                 140
Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser Leu Gln
145                 150                 155                 160
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His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys Gly Asn
                165                 170                 175
Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn Val Ser
            180                 185                 190
Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly Ala Ile
        195                 200                 205
Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu Phe Phe
    210                 215                 220
Thr Gly Asn Ser Ala Thr Asn Gly Gly Ala Ile Cys Cys Ile Ser Asp
225                 230                 235                 240
Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn Gln Glu
                245                 250                 255
Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala Ile Tyr
            260                 265                 270
Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe Ile Asn
        275                 280                 285
Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly Gly Ser
    290                 295                 300
Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn Asn Ser
305                 310                 315                 320
Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr Leu Xaa
                325                 330                 335
Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp Ile Leu
            340                 345                 350
Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser Pro Leu
        355                 360                 365
Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala Thr Ala
    370                 375                 380
Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile Phe Ser
385                 390                 395                 400
Ser Glu Arg Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu Thr Ser
                405                 410                 415
Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val Leu Lys
            420                 425                 430
Asp Arg Ala Val Leu Ser Ala Pro Ser Leu Ser Gln Asp Pro Gln Ala
        435                 440                 445
Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Ser Asp Leu
    450                 455                 460
Lys Leu Ala Thr Leu Ser Ile Pro Leu His Ser Leu Asp Thr Glu Lys
465                 470                 475                 480
Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile Phe Leu
                485                 490                 495
Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu Leu Ser
            500                 505                 510
Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu Gln Ser
        515                 520                 525
His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln
    530                 535                 540
Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu
545                 550                 555                 560
Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln
                565                 570                 575
Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln
            580                 585                 590
Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala Tyr Leu
        595                 600                 605
Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val His Asp
    610                 615                 620
Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr
625                 630                 635                 640
Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu
```

```
                645                 650                 655
Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser
            660                 665                 670
Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr
        675                 680                 685
Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His
    690                 695                 700
Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser
705                 710                 715                 720
Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile
                725                 730                 735
Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys
            740                 745                 750
Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly
        755                 760                 765
Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro
    770                 775                 780
Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr
785                 790                 795                 800
Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser
                805                 810                 815
Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met
            820                 825                 830
Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg
        835                 840                 845
Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg
    850                 855                 860
Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe
865                 870                 875                 880

<210> 176
<211> 982
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 981
<223> Xaa = Any Amino Acid

<400> 176
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Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala
            20                  25                  30
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro
        35                  40                  45
Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg
    50                  55                  60
Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala
65                  70                  75                  80
Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe
                85                  90                  95
Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro
            100                 105                 110
Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Thr Ser Thr
        115                 120                 125
Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Leu Asn
    130                 135                 140
Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly
145                 150                 155                 160
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Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys
                165                 170                 175
Val Phe Gln Glu Asn Thr Ala Gln Ala Asp Gly Gly Ala Cys Gln Val
            180                 185                 190
Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val
        195                 200                 205
Ala Asn Val Ala Gly Val Arg Gly Gly Gly Ile Ala Ala Val Gln Asp
    210                 215                 220
Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val
225                 230                 235                 240
Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg
                245                 250                 255
Val Gly Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn
            260                 265                 270
Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala
        275                 280                 285
Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr
    290                 295                 300
Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser
305                 310                 315                 320
Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe
                325                 330                 335
Ser Ser Asn Val Ala Ala Gly Lys Gly Gly Ala Ile Tyr Ala Lys Lys
            340                 345                 350
Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala
        355                 360                 365
Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu
    370                 375                 380
Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr
385                 390                 395                 400
Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln
                405                 410                 415
Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys
            420                 425                 430
Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly
        435                 440                 445
Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly
    450                 455                 460
Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu
465                 470                 475                 480
Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys
                485                 490                 495
Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr
            500                 505                 510
Met Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln
        515                 520                 525
Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu
    530                 535                 540
Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr
545                 550                 555                 560
Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr
                565                 570                 575
Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp
            580                 585                 590
Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile
        595                 600                 605
Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro
    610                 615                 620
Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly
625                 630                 635                 640
Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr
```

```
                645                 650                 655
Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu
            660                 665                 670
Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp
        675                 680                 685
Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser
    690                 695                 700
Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His
705                 710                 715                 720
Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr
                725                 730                 735
Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala
            740                 745                 750
Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser
        755                 760                 765
Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala
    770                 775                 780
Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr
785                 790                 795                 800
Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu
                805                 810                 815
Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala
            820                 825                 830
Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu
        835                 840                 845
Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe
    850                 855                 860
Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu
865                 870                 875                 880
Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr
                885                 890                 895
His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr
            900                 905                 910
Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr
        915                 920                 925
Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg
    930                 935                 940
Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His
945                 950                 955                 960
Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala
                965                 970                 975
Gly Ser Lys Val Xaa Phe
            980

<210> 177
<211> 964
<212> PRT
<213> Chlamydia

<400> 177
Met Lys Lys Ala Phe Phe Phe Leu Ile Gly Asn Ser Leu Ser Gly
 1               5                  10                  15
Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val
            20                  25                  30
Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly
        35                  40                  45
Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile
    50                  55                  60
Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile
65                  70                  75                  80
Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe
```

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                        85                  90                  95
Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser
            100                 105                 110
Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile
        115                 120                 125
Phe Glu Asn Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr
    130                 135                 140
Ala Ala Asp Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu
145                 150                 155                 160
Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser
                165                 170                 175
Tyr Val Gln Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser
            180                 185                 190
Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr
        195                 200                 205
Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser
    210                 215                 220
Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys
225                 230                 235                 240
Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg
                245                 250                 255
Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr
            260                 265                 270
Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg
        275                 280                 285
Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile
    290                 295                 300
Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val
305                 310                 315                 320
Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly
                325                 330                 335
Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp
            340                 345                 350
Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn
        355                 360                 365
Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile
    370                 375                 380
Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser
385                 390                 395                 400
Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val
                405                 410                 415
Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe
            420                 425                 430
Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln
        435                 440                 445
Thr Lys Thr Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile
    450                 455                 460
Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly
465                 470                 475                 480
Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly
                485                 490                 495
Thr Gly Asp Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly
            500                 505                 510
Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu
        515                 520                 525
Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala
    530                 535                 540
Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr
545                 550                 555                 560
Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser
                565                 570                 575
```

```
Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser
            580                 585                 590
Glu Asn Ile Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln
        595                 600                 605
Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala
    610                 615                 620
Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg
625                 630                 635                 640
Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys
                645                 650                 655
His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu
            660                 665                 670
Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His
        675                 680                 685
Pro Phe Trp Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln
    690                 695                 700
Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr
705                 710                 715                 720
Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe
                725                 730                 735
Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val
            740                 745                 750
Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln
        755                 760                 765
Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp
    770                 775                 780
His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln
785                 790                 795                 800
Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu
                805                 810                 815
Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu
            820                 825                 830
Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly
        835                 840                 845
Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu
    850                 855                 860
Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro
865                 870                 875                 880
Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln
                885                 890                 895
Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe
            900                 905                 910
Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser
        915                 920                 925
Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His
    930                 935                 940
Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile
945                 950                 955                 960
Ala Leu Arg Phe


<210> 178
<211> 1530
<212> PRT
<213> Chlamydia

<400> 178
Met Ser Ser Glu Lys Asp Ile Lys Ser Thr Cys Ser Lys Phe Ser Leu
 1               5                  10                  15
Ser Val Val Ala Ala Ile Leu Ala Ser Val Ser Gly Leu Ala Ser Cys
            20                  25                  30
```

```
Val Asp Leu His Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val
        35                  40                  45
Gly Pro Gln Ala Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val
    50                  55                  60
Gly Ser Lys Asp Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly
65                  70                  75                  80
Asp Pro Ser Ser Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys
                85                  90                  95
Val Glu Gln Ser Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln
            100                 105                 110
Gly Val Asp Gln Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser
        115                 120                 125
Phe Thr Ser Ser Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu
    130                 135                 140
Gly Ile Ala Phe Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr
145                 150                 155                 160
Asp Val Lys Ala Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp
                165                 170                 175
Leu Ile Phe Glu Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser
            180                 185                 190
Ser Leu Glu Gln Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His
        195                 200                 205
Asp Cys Gln Gly Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala
    210                 215                 220
Glu Gly Ser Ser Ala Asn Asp His Leu Gly Phe Gly Gly Gly Ala Phe
225                 230                 235                 240
Phe Val Thr Gly Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala
                245                 250                 255
Gly Asp Met Val Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly
            260                 265                 270
Asn Ser Ala Asn Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys
        275                 280                 285
Val Leu Phe Val Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg
    290                 295                 300
Ala Leu Ser Gly Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln
305                 310                 315                 320
Asn Cys Ala Glu Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu
                325                 330                 335
Asp Lys Gly Ser Leu Gly Gly Gly Ala Ile Ser Ser Leu Gly Thr Val
            340                 345                 350
Leu Leu Gln Gly Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala
        355                 360                 365
Ser Gln Gly Gly Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn
    370                 375                 380
Glu Gly Pro Val Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Gly
385                 390                 395                 400
Ala Ile Ala Ala Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly
                405                 410                 415
Ile Ser Phe Glu Gly Gly Lys Ala Ser Phe Gly Gly Gly Ile Ala Cys
            420                 425                 430
Gly Ser Phe Ser Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp
        435                 440                 445
Ile Ser Lys Asn Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr
    450                 455                 460
Thr Ser Asp Leu Gly Gln Met Glu Tyr Gln Gly Gly Gly Ala Leu Phe
465                 470                 475                 480
Gly Glu Asn Ile Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys
                485                 490                 495
Asp Asn Ile Val Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly
            500                 505                 510
Gly Ala Ile Leu Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly
```

```
        515                 520                 525
Gly Ile Ser Phe Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr
    530                 535                 540
Gln Glu Glu Phe Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser
545                 550                 555                 560
Ser Gly Tyr Ser Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile
                565                 570                 575
Leu His Asn Ala Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser
            580                 585                 590
Glu Glu Glu Ala Thr Leu Leu Gly Cys Cys Gly Gly Gly Ala Val His
        595                 600                 605
Gly Met Asp Ser Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly
    610                 615                 620
Asn Asn Tyr Ala Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser
625                 630                 635                 640
Lys Thr Val Gln Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn
                645                 650                 655
Ile Ala Ser Leu Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys
            660                 665                 670
Glu Leu Val Asp Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg
        675                 680                 685
Val Tyr Gly Gly Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser
    690                 695                 700
Gly Asn Lys Gly Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu
705                 710                 715                 720
Tyr Val Glu Glu Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro
                725                 730                 735
Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln
            740                 745                 750
Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly
        755                 760                 765
Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg
    770                 775                 780
Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala Lys Arg Val Arg Ile Val
785                 790                 795                 800
Asp Asn Gln Glu Ala Val Val Phe Ser Asn Asn Phe Ser Asp Ile Tyr
                805                 810                 815
Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg Glu Glu Asp Lys Leu Asp
            820                 825                 830
Gly Gln Ile Pro Glu Val Leu Ile Ser Gly Asn Ala Gly Asp Val Val
        835                 840                 845
Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu His Leu Pro His Thr Gly
    850                 855                 860
Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr Ile Ser Gln Asn Thr Gly
865                 870                 875                 880
Asn Val Leu Phe Tyr Asn Asn Val Ala Cys Ser Gly Gly Ala Val Arg
                885                 890                 895
Ile Glu Asp His Gly Asn Val Leu Leu Glu Ala Phe Gly Gly Asp Ile
            900                 905                 910
Val Phe Lys Gly Asn Ser Ser Phe Arg Ala Gln Gly Ser Asp Ala Ile
        915                 920                 925
Tyr Phe Ala Gly Lys Glu Ser His Ile Thr Ala Leu Asn Ala Thr Glu
    930                 935                 940
Gly His Ala Ile Val Phe His Asp Ala Leu Val Phe Glu Asn Leu Lys
945                 950                 955                 960
Glu Arg Lys Ser Ala Glu Val Leu Leu Ile Asn Ser Arg Glu Asn Pro
                965                 970                 975
Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu Ala Glu Ser Lys Val Pro
            980                 985                 990
Gln Cys Ile His Val Gln Gln Gly Ser Leu Glu Leu Leu Asn Gly Ala
        995                 1000                1005
```

```
Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val
    1010                1015                1020
Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val
1025                1030                1035                1040
Gln Gly His Ala Ile Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser
                1045                1050                1055
Glu Pro Glu Gly Ala His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr
            1060                1065                1070
Thr Val Pro Met Val Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser
        1075                1080                1085
Phe Ser Ser Ser Gln Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile
    1090                1095                1100
Val Pro Gly Gly Ser Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu
1105                1110                1115                1120
Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn
                1125                1130                1135
Glu Ala Lys Val Pro Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala
            1140                1145                1150
Ser Ala Glu Ile Ser Asn Leu Ser Val Ser Asp Leu Gln Ile His Val
        1155                1160                1165
Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp
    1170                1175                1180
Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro
1185                1190                1195                1200
Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn
                1205                1210                1215
Ala Leu Trp Glu Glu Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg
            1220                1225                1230
Phe Ala His Asn Leu Thr Ala Gln Arg Met Glu Phe Asp Tyr Ser Thr
        1235                1240                1245
Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr Leu Ser Ala Glu
    1250                1255                1260
Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr Gly Gly Ala Ser
1265                1270                1275                1280
Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val Leu Gly Val Ser
                1285                1290                1295
Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys Phe Asp Ala Glu
            1300                1305                1310
Val Ser Arg Lys Gly Val Val Gly Ser Val Tyr Thr Gly Phe Leu Ala
        1315                1320                1325
Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser Leu Gly Glu Thr Gln Asn
    1330                1335                1340
Asp Met Lys Thr Arg Tyr Gly Val Leu Gly Glu Ser Ser Ala Ser Trp
1345                1350                1355                1360
Thr Ser Arg Gly Val Leu Ala Asp Ala Leu Val Glu Tyr Arg Ser Leu
                1365                1370                1375
Val Gly Pro Val Arg Pro Thr Phe Tyr Ala Leu His Phe Asn Pro Tyr
            1380                1385                1390
Val Glu Val Ser Tyr Ala Ser Met Lys Phe Pro Gly Phe Thr Glu Gln
        1395                1400                1405
Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala Ser Leu Thr Asn Ile Thr
    1410                1415                1420
Ile Pro Leu Gly Met Lys Phe Glu Leu Ala Phe Ile Lys Gly Gln Phe
1425                1430                1435                1440
Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr Ala Trp Glu Ala Tyr Arg
                1445                1450                1455
Lys Val Glu Gly Gly Ala Val Gln Leu Leu Glu Ala Gly Phe Asp Trp
            1460                1465                1470
Glu Gly Ala Pro Met Asp Leu Pro Arg Gln Glu Leu Arg Val Ala Leu
        1475                1480                1485
Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe Ser Thr Val Leu Gly Leu
```

```
    1490                    1495                    1500
Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr Asp Ser Lys Leu Gly Tyr
1505                1510                1515                1520
Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe
                1525                1530
```

<210> 179
<211> 1776
<212> PRT
<213> Chlamydia

<400> 179

```
Ala Ile Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val Leu
 1               5                  10                  15
Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr
            20                  25                  30
Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe Thr
        35                  40                  45
Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val
    50                  55                  60
Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg Lys His Leu
65                  70                  75                  80
Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser
                85                  90                  95
Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser Ser
            100                 105                 110
Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn Gly Gly Ile
        115                 120                 125
Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu
    130                 135                 140
Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Phe Gly Glu
145                 150                 155                 160
Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala
                165                 170                 175
Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu
            180                 185                 190
Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val Tyr Ala Lys
        195                 200                 205
Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn
    210                 215                 220
Gly Gly Glu Gln Gly Gly Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu
225                 230                 235                 240
Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala
                245                 250                 255
Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Leu Thr
            260                 265                 270
Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu
        275                 280                 285
Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr
    290                 295                 300
Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp
305                 310                 315                 320
Asp Val Leu Gly Lys Gly Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr
                325                 330                 335
Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr
            340                 345                 350
Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn
        355                 360                 365
Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly
    370                 375                 380
Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu
```

```
385                 390                 395                 400
Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser Glu Asn
                405                 410                 415
Thr Ala Lys Gly His Gly Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu
            420                 425                 430
Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser
        435                 440                 445
Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr Asp Thr
    450                 455                 460
Pro Glu Ser Ser Thr Pro Ser Ser Ser Ser Pro Ala Ser Thr Pro Glu
465                 470                 475                 480
Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu
                485                 490                 495
Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln
            500                 505                 510
Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn
        515                 520                 525
Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly
    530                 535                 540
Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu
545                 550                 555                 560
Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr
                565                 570                 575
Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn
            580                 585                 590
Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu
        595                 600                 605
Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala
    610                 615                 620
Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu
625                 630                 635                 640
Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly
                645                 650                 655
Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp
            660                 665                 670
Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr
        675                 680                 685
Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn
    690                 695                 700
Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn
705                 710                 715                 720
Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser
                725                 730                 735
Val Ser Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly
            740                 745                 750
Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn
        755                 760                 765
Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val
    770                 775                 780
Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp Asn Pro Asp
785                 790                 795                 800
Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly Pro Thr Glu
                805                 810                 815
Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile Gly Gly Gly
            820                 825                 830
Ala Ile Tyr Gly Glu Thr Val Lys Ile Glu Asn Phe Ser Gly Gln Gly
        835                 840                 845
Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser
    850                 855                 860
Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe
865                 870                 875                 880
```

```
Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr Phe Ser Gly Asn
                885                 890                 895
Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala Gly Gly Ala Ile
            900                 905                 910
Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val Phe Ser Lys Asn
        915                 920                 925
Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr Gln Arg Lys Asp
    930                 935                 940
Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val Ser Leu Ser Gly
945                 950                 955                 960
Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly Ser Ala Ile Gly
                965                 970                 975
Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys Leu Glu Ser Gly
            980                 985                 990
Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr
        995                 1000                1005
Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn
    1010                1015                1020
Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser
1025                1030                1035                1040
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Leu Val Thr Pro
                1045                1050                1055
Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp
            1060                1065                1070
Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn
        1075                1080                1085
Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly
    1090                1095                1100
Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr
1105                1110                1115                1120
Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val Lys Leu Thr Met
                1125                1130                1135
Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr
            1140                1145                1150
Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp
        1155                1160                1165
Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser Ala Phe Thr Gly
    1170                1175                1180
Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro
1185                1190                1195                1200
Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu Lys Pro Asn Thr
                1205                1210                1215
Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly Ser Ser Leu Val
            1220                1225                1230
Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val Ala Asp Gly Ala
        1235                1240                1245
Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser Val Glu Lys Asn
    1250                1255                1260
Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile
1265                1270                1275                1280
Asp Thr Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser Thr Asp Ser Glu
                1285                1290                1295
Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn Asn Asn Asp Ala
            1300                1305                1310
Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser Pro Ala Val Ala
        1315                1320                1325
Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala Ala Ala Thr Ala
    1330                1335                1340
Thr Pro Thr Thr Thr Pro Thr Ala Thr Thr Thr Thr Ser Asn Gln Val
1345                1350                1355                1360
Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe
```

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                    1365                1370                1375
Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser Leu Leu Val Leu
                1380                1385                1390
Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile Val Leu Thr Gly
            1395                1400                1405
Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro
        1410                1415                1420
Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp Lys Phe Asp Ser
1425                1430                1435                1440
Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His Phe Tyr Ala Asn
                    1445                1450                1455
Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val Lys Gln Gly Leu
                1460                1465                1470
Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu Val Ser Tyr Asn
            1475                1480                1485
Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser Gln Val Gly Thr
        1490                1495                1500
Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala
1505                1510                1515                1520
Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly Ala Ala Phe Ser
                    1525                1530                1535
Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr
                1540                1545                1550
His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys
            1555                1560                1565
Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu
        1570                1575                1580
Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys His Asp Thr Val
1585                1590                1595                1600
Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly Glu Trp Glu Asp
                    1605                1610                1615
Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val Leu Arg Thr Pro
                1620                1625                1630
Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr
            1635                1640                1645
Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg
        1650                1655                1660
Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu
1665                1670                1675                1680
Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg
                    1685                1690                1695
Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn Ser Pro Thr Cys
                1700                1705                1710
Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu Ile Ile Cys Gly
            1715                1720                1725
Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr
        1730                1735                1740
Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp
1745                1750                1755                1760
Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala Arg Met Thr Phe
                    1765                1770                1775
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<211> 1752
<212> PRT
<213> Chlamydia

<400> 180

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Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Glu Leu Asn Phe Ser Arg
```

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Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile Gly Glu Ala
        35                      40                      45
Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr
    50                      55                      60
Asn Ile Pro Thr Thr Asp Thr Thr Thr Pro Thr Asn Ser Asn Ser Ser
65                      70                      75                      80
Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr
                85                      90                      95
Thr Thr Thr Pro Asp Pro Lys Gly Gly Gly Ala Phe Tyr Asn Ala His
            100                     105                     110
Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu
        115                     120                     125
Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Gly Ala Ile Phe Ser
    130                     135                     140
Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr Ile Gln Asn
145                     150                     155                     160
Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Gly Ser Thr Ile
                165                     170                     175
Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn Ser Ala Glu
            180                     185                     190
Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala
        195                     200                     205
Ser Glu Thr Ser Gly Ser Ser Ser Ser Ser Gly Asn Asp Ser Val Ser
    210                     215                     220
Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Ala Asn Leu Gln Ser
225                     230                     235                     240
His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu
                245                     250                     255
Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala
            260                     265                     270
Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile
        275                     280                     285
Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val
    290                     295                     300
Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu
305                     310                     315                     320
Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser
                325                     330                     335
Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly Gly
            340                     345                     350
Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu Glu Glu Ile
        355                     360                     365
Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr
    370                     375                     380
Leu Pro Ser Leu Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp
385                     390                     395                     400
Ala Ser Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asp
                405                     410                     415
Ser Gly Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val
            420                     425                     430
Pro Val Thr Ala Lys Gly Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser
        435                     440                     445
Ile Thr Asn Ile Thr Gly Ile Ile Glu Ile Ala Asn Asn Lys Ala Thr
    450                     455                     460
Asp Val Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn
465                     470                     475                     480
Ser His Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly
                485                     490                     495
Gly Ile Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys
            500                     505                     510
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Thr Leu Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Gly Leu Phe
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Ile Lys Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe
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Cys Leu Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val
545                 550                 555                 560
Thr Lys Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro
                565                 570                 575
Gly Ile Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser
            580                 585                 590
Thr Gly Gly Asn Gly Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser
        595                 600                 605
Asn Leu Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly
    610                 615                 620
Gly Gly Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala
625                 630                 635                 640
Glu Gln Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala
                645                 650                 655
Pro Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser
            660                 665                 670
Leu Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn
        675                 680                 685
Lys Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr
    690                 695                 700
Val Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly
705                 710                 715                 720
Ile Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile
                725                 730                 735
Ser Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu
            740                 745                 750
Ser Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu
        755                 760                 765
Val Gly Lys Glu Gly Gly Gly Leu His Ala Lys Thr Val Asn Ile Ser
    770                 775                 780
Asn Leu Lys Ser Gly Phe Ser Phe Ser Asn Asn Lys Ala Asn Ser Ser
785                 790                 795                 800
Ser Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala Ala
                805                 810                 815
Ser Leu Gln Ala Ala Ala Ala Ala Ala Pro Ser Ser Pro Ala Thr Pro
            820                 825                 830
Thr Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr
        835                 840                 845
Phe Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile
    850                 855                 860
Asp Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile
865                 870                 875                 880
Tyr Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser
                885                 890                 895
Tyr Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr
            900                 905                 910
Gly Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn
        915                 920                 925
Cys Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Ile Ala Thr Pro Lys
    930                 935                 940
Thr Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile
945                 950                 955                 960
Gly Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg
                965                 970                 975
Phe Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala
            980                 985                 990
Asn Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr
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Glu Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln
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Ala Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly
1025 1030 1035 1040
Asn Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala
1045 1050 1055
Ile Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu
1060 1065 1070
Phe Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser
1075 1080 1085
Gly Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp
1090 1095 1100
Pro Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu
1105 1110 1115 1120
Ala Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn
1125 1130 1135
Gln Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val
1140 1145 1150
Lys Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp
1155 1160 1165
Cys Val His Thr Ser Thr Lys Lys Thr Gly Ser Thr Gln Asn Val Tyr
1170 1175 1180
Glu Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly
1185 1190 1195 1200
Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro
1205 1210 1215
Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr
1220 1225 1230
Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile
1235 1240 1245
Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala
1250 1255 1260
Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro
1265 1270 1275 1280
Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr
1285 1290 1295
Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr
1300 1305 1310
Asn Pro Lys Arg Ile Ser Ala Ala Val Pro Ser Gly Ser Ala Ala Thr
1315 1320 1325
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1330 1335 1340
Leu Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser
1345 1350 1355 1360
Asp Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val
1365 1370 1375
Gln Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly
1380 1385 1390
Tyr Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu
1395 1400 1405
Gln Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro
1410 1415 1420
Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser
1425 1430 1435 1440
Met Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala
1445 1450 1455
Arg Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly
1460 1465 1470
Thr Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr
1475 1480 1485

Tyr Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp
    1490   1495   1500
Phe Ile Leu Gly Ala Ala Phe Ser Lys Ile Val Gly Lys Thr Lys Ala
1505   1510   1515   1520
Ile Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr
                1525   1530   1535
Gln Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys
            1540   1545   1550
Gln His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr
        1555   1560   1565
Gly His Ile Lys His Asp Thr Thr Thr Leu Tyr Pro Ser Ile His Glu
    1570   1575   1580
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1585   1590   1595   1600
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                1605   1610   1615
Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe
            1620   1625   1630
Thr Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg
        1635   1640   1645
Asn Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn
    1650   1655   1660
Cys Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser
1665   1670   1675   1680
Ile Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn
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Glu Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Ala Arg
            1700   1705   1710
Ala Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr
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Gly Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr
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1745   1750

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<212> DNA
<213> Chlamydia

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<210> 182
<211> 3021
<212> DNA
<213> Chlamydia

<400> 182

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ccctatactg ttataggaga tccgagtggg actactgttt tttctgcagg agagttaaca     180
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<212> DNA
<213> Chlamydia

<400> 183

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ggagacactc acaatctcac taactgctat ctcgataacc tacgctacat actggctatt     240
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tggcaagtag gcctcgccct gtcttacaga ttgaatatgc ttgttccata tattggcgta     1260
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aactggtcaa gagcaacttt tgatgctgat actatccgca ttgctcaacc taaattaaaa 1320
tcggagattc ttaacattac tacatggaac ccaagcctta taggatcaac cactgctttg 1380
cccaataata gtggtaagga tgttctatct gatgtcttgc aaattgcttc gattcagatc 1440
aacaaaatga agtctagaaa agcttgtggt gtagctgttg gtgcaacgtt aatcgacgct 1500
gacaaatggt caatcactgg tgaagcacgc ttaatcaatg aaagagctgc tcacatgaat 1560
gcacaattcc gcttctaa 1578

<210> 189
<211> 866
<212> PRT
<213> Chlamydia

<220>
<221> VARIANT
<222> 220, 242, 425, 448, 453, 455
<223> Xaa = Any Amino Acid

<400> 189
Met Ala Ser His His His His His His Leu Phe Gly Gln Asp Pro Leu
1 5 10 15
Gly Glu Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr
20 25 30
Phe Phe Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala
35 40 45
His Ala Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys
50 55 60
Trp Phe Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe
65 70 75 80
Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe
85 90 95
Thr Asp Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys
100 105 110
Asn Gly Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg
115 120 125
Asn His Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser
130 135 140
Leu Gln His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys
145 150 155 160
Gly Asn Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn
165 170 175
Val Ser Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly
180 185 190
Ala Ile Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu
195 200 205
Phe Phe Thr Gly Asn Ser Ala Thr Asn Gly Gly Xaa Ile Cys Cys Ile
210 215 220
Ser Asp Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn
225 230 235 240
Gln Xaa Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala
245 250 255
Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe
260 265 270
Ile Asn Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly
275 280 285
Gly Ser Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn
290 295 300
Asn Ser Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr
305 310 315 320
Leu Glu Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp
325 330 335
Ile Leu Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Ser Lys Glu Ser

340 345 350
Pro Leu Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala
355 360 365
Thr Ala Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile
370 375 380
Phe Ser Ser Glu Arg Leu Ser Glu Glu Glu Lys Thr Pro Asp Asn Leu
385 390 395 400
Thr Ser Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val
405 410 415
Leu Lys Asp Arg Ala Val Leu Ser Xaa Pro Ser Leu Ser Gln Asp Pro
420 425 430
Gln Ala Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Xaa
435 440 445
Asp Leu Lys Leu Xaa Thr Xaa Ser Ile Pro Leu His Ser Leu Asp Thr
450 455 460
Glu Lys Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile
465 470 475 480
Phe Leu Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu
485 490 495
Leu Ser Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu
500 505 510
Gln Ser His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly
515 520 525
Tyr Gln Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His
530 535 540
Ser Leu Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu
545 550 555 560
Arg Gln Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp
565 570 575
Met Gln Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala
580 585 590
Tyr Leu Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val
595 600 605
His Asp Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu
610 615 620
Gly Tyr Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe
625 630 635 640
Cys Leu Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile
645 650 655
Thr Ser Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu
660 665 670
Ala Thr Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser
675 680 685
Ile His Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe
690 695 700
Gly Ser Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile
705 710 715 720
Pro Ile Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe
725 730 735
Ser Lys Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser
740 745 750
Ser Gly Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser
755 760 765
Leu Pro Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr
770 775 780
Tyr Tyr Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val
785 790 795 800
Glu Ser Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala
805 810 815
Pro Met Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn
820 825 830

Gln Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val
835 840 845
Leu Arg Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr
850 855 860
Arg Phe
865

<210> 190
<211> 1006
<212> PRT
<213> Chlamydia

<400> 190
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
1 5 10 15
Val Pro His His His His His His Met Ile Pro Gln Gly Ile Tyr Asp
20 25 30
Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro
35 40 45
Ser Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu
50 55 60
Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu
65 70 75 80
Gly Ser Phe Thr Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn
85 90 95
Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp
100 105 110
Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys
115 120 125
Asn Ser Leu Leu Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser
130 135 140
Gln Thr Pro Thr Thr Thr Ser Thr Pro Ser Asn Gly Thr Ile Tyr Ser
145 150 155 160
Lys Thr Asp Leu Leu Leu Leu Asn Asn Glu Lys Phe Ser Phe Tyr Ser
165 170 175
Asn Leu Val Ser Gly Asp Gly Gly Ala Ile Asp Ala Lys Ser Leu Thr
180 185 190
Val Gln Gly Ile Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln
195 200 205
Ala Asp Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala
210 215 220
Asn Glu Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly
225 230 235 240
Gly Gly Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser
245 250 255
Thr Ser Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val
260 265 270
Glu Phe Asp Gly Asn Val Ala Arg Val Gly Gly Gly Ile Tyr Ser Tyr
275 280 285
Gly Asn Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn
290 295 300
Val Ala Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln
305 310 315 320
Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys
325 330 335
Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe
340 345 350
Asp Gly Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys
355 360 365
Gly Gly Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro
370 375 380

Val Gln Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu
385 390 395 400
Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile
405 410 415
Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val
420 425 430
Asn Gly Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly
435 440 445
Lys Ile Thr Thr Leu Arg Ala Lys Ala Gly His Gln Ile Leu Phe Asn
450 455 460
Asp Pro Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser
465 470 475 480
Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val
485 490 495
Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln
500 505 510
Gly Arg Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu
515 520 525
Ser Gln Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Leu Asp
530 535 540
Phe Val Thr Pro Gln Pro Pro Gln Gln Pro Pro Ala Ala Asn Gln Leu
545 550 555 560
Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn
565 570 575
Asn Ala Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His
580 585 590
Pro Ala Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly
595 600 605
Pro Ile Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp
610 615 620
Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly
625 630 635 640
Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu
645 650 655
Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro
660 665 670
Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys
675 680 685
Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu Val Pro Asn
690 695 700
Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His Ser Ala Ile
705 710 715 720
Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser
725 730 735
Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly
740 745 750
Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe
755 760 765
Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser
770 775 780
Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser
785 790 795 800
Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly
805 810 815
Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys
820 825 830
Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn
835 840 845
Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro
850 855 860
Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe

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865                 870                 875                 880
Ser Tyr Ala Asp His Glu Ser Phe Thr Glu Glu Gly Asp Gln Ala Arg
                885                 890                 895
Ala Phe Lys Ser Gly His Leu Leu Asn Leu Ser Val Pro Val Gly Val
            900                 905                 910
Lys Phe Asp Arg Cys Ser Ser Thr His Pro Asn Lys Tyr Ser Phe Met
        915                 920                 925
Ala Ala Tyr Ile Cys Asp Ala Tyr Arg Thr Ile Ser Gly Thr Glu Thr
    930                 935                 940
Thr Leu Leu Ser His Gln Glu Thr Trp Thr Thr Asp Ala Phe His Leu
945                 950                 955                 960
Ala Arg His Gly Val Val Val Arg Gly Ser Met Tyr Ala Ser Leu Thr
                965                 970                 975
Ser Asn Ile Glu Val Tyr Gly His Gly Arg Tyr Glu Tyr Arg Asp Ala
            980                 985                 990
Ser Arg Gly Tyr Gly Leu Ser Ala Gly Ser Lys Val Arg Phe
        995                 1000                1005

&lt;210&gt; 191
&lt;211&gt; 977
&lt;212&gt; PRT
&lt;213&gt; Chlamydia

&lt;400&gt; 191
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu
 1               5                  10                  15
Val Pro Ser Ser Asp Pro His His His His His His Gly Leu Ala Arg
            20                  25                  30
Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro
        35                  40                  45
Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly Asp Thr His
    50                  55                  60
Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile Leu Ala Ile
65                  70                  75                  80
Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile Thr Asp Tyr
                85                  90                  95
Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe Ala Lys Asn
            100                 105                 110
Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser Pro Asn Ser
        115                 120                 125
Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile Phe Glu Asn
    130                 135                 140
Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr Ala Ala Asp
145                 150                 155                 160
Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu Tyr Ile Asn
                165                 170                 175
His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser Tyr Val Gln
            180                 185                 190
Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser Glu Asn Gln
        195                 200                 205
Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr Asn Thr Ala
    210                 215                 220
Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe Glu Ser
225                 230                 235                 240
Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala Gly Gly
                245                 250                 255
Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly Asn Ile
            260                 265                 270
Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr Ala Ser Ser
        275                 280                 285
Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg Leu Asp Val
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    290                 295                 300
Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn
305                 310                 315                 320
Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly
                325                 330                 335
Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile
            340                 345                 350
Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala
        355                 360                 365
Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly
    370                 375                 380
Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala
385                 390                 395                 400
Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu
                405                 410                 415
Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser
            420                 425                 430
Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala
        435                 440                 445
Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr
    450                 455                 460
Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His
465                 470                 475                 480
Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser
                485                 490                 495
Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly Thr Gly Asp
            500                 505                 510
Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly Leu Asn Leu
        515                 520                 525
Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu Trp Val Glu
    530                 535                 540
Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala Ala Thr Phe
545                 550                 555                 560
Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr Gly Asn Ser
                565                 570                 575
Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser Gln Pro Met
            580                 585                 590
Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser Glu Asn Ile
        595                 600                 605
Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln Gly Leu Trp
    610                 615                 620
Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala
625                 630                 635                 640
Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu
                645                 650                 655
Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys His Arg Ser
            660                 665                 670
Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu Ala Thr Glu
        675                 680                 685
Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His Pro Phe Trp
    690                 695                 700
Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr Gln Asp Pro Arg
705                 710                 715                 720
Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr Ser Ala Gly
                725                 730                 735
Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe Ser Gln Thr
            740                 745                 750
Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val Ser Ser Lys
        755                 760                 765
Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln Glu Gly Phe
    770                 775                 780
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Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp His Asn Cys
785 790 795 800
His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln Gly Thr Phe
805 810 815
Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu Pro Met Lys
820 825 830
Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu Gly Ala Leu
835 840 845
Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly Ala Tyr Pro
850 855 860
Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu Val Pro Ile
865 870 875 880
Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro Gln Ala Trp
885 890 895
Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln Glu Pro Gly
900 905 910
Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe Gly Ser Gly
915 920 925
Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser Gln Gln Thr
930 935 940
Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His Gly Phe Tyr
945 950 955 960
Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile Ala Leu Arg
965 970 975
Phe

<210> 192
<211> 848
<212> PRT
<213> Chlamydia

<400> 192
Met Ala Ser His His His His His His Gly Ala Ile Ser Cys Leu Arg
1 5 10 15
Gly Asp Val Val Ile Ser Gly Asn Lys Gly Arg Val Glu Phe Lys Asp
20 25 30
Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu Thr Val Glu Lys Val Glu
35 40 45
Glu Val Glu Pro Ala Pro Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe
50 55 60
Leu Gly Ser Val Glu Gln Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu
65 70 75 80
Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser
85 90 95
Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala
100 105 110
Lys Arg Val Arg Ile Val Asp Asn Gln Glu Ala Val Val Phe Ser Asn
115 120 125
Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg
130 135 140
Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu Val Leu Ile Ser Gly
145 150 155 160
Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu
165 170 175
His Leu Pro His Thr Gly Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr
180 185 190
Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr Asn Asn Val Ala Cys
195 200 205
Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly Asn Val Leu Leu Glu
210 215 220